

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Waeber T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carrinco P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
CC -!- FUNCTION: Cooperates with LY96 and TLR6 to mediate the innate
CC immune response to bacterial lipoproteins and other microbial cell
CC wall components. Acts via MyD88 and TRAF6, leading to NF-kappa-B
CC activation, cytokine secretion and the inflammatory response. May
CC also promote apoptosis in response to lipoproteins (By
CC similarity).
CC -!- SUBUNIT: Binds LY96 and TLR6 via the extracellular domain. Binds
CC MyD88 via their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosome.
CC -!- TISSUE SPECIFICITY: Detected in a macrophage cell line, smooth
CC muscle, lung, spleen, thymus, brain and adipose tissue.
CC -!- PM: N-glycosylated.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC -!- SIMILARITY: Contains 1 TIR domain.
CC -!- SIMILARITY: Contains 16 leucine-rich (LRR) repeats.
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CC -----
DR EMBL; AF185284; AAF04277.1; -;
DR EMBL; AF124741; AAD46481.1; -;
DR EMBL; AF216289; AAF28345.1; -;
DR EMBL; AF165189; AAD49335.1; -;
DR EMBL; AK005043; BAB23770.1; -;
DR HSPB; O60603; 1FYW
DR MGD; MGI:1346060; Tlr2.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNRI1P.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
DR Transmembrane; Repeat; Inflammatory response; Signal;
KW Receptor; Immune response; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 24 POTENTIAL. RECEPTOR 2.
FT CHAIN 25 784 TOLL-LIKE RECEPTOR 2.
FT DOMAIN 25 587 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 588 608 POTENTIAL.
FT DOMAIN 609 784 CYTOPLASMIC (POTENTIAL).
FT REPEAT 51 74 LRR 1.
FT REPEAT 75 98 LRR 2.

FT REPEAT 99 122 LRR 3.
FT REPEAT 124 147 LRR 4.
FT REPEAT 173 196 LRR 5.
FT REPEAT 221 244 LRR 6.
FT REPEAT 276 300 LRR 7.
FT REPEAT 335 358 LRR 8.
FT REPEAT 359 384 LRR 9.
FT REPEAT 386 411 LRR 10.
FT REPEAT 412 436 LRR 11.
FT REPEAT 438 456 LRR 12.
FT REPEAT 457 476 LRR 13.
FT REPEAT 477 500 LRR 14.
FT REPEAT 502 521 LRR 15.
FT REPEAT 522 548 LRR 16.
FT DOMAIN 639 784 TIR.
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 681 681 P-SH: ABOLISHES MYD88-BINDING AND
FT RESPONSE TO MICROBIAL CELL WALL
FT COMPONENTS.
FT CONFLICT 59 59 L -> P (IN REF. 5).
FT CONFLICT 82 82 I -> M (IN REF. 5).
FT SEQUENCE 784 AA; 89448 MW; 606D56BF85F320A2 CRC64;
Query Match 7.1%; Score 130.5; DB 1; Length 784;
Best Local Similarity 21.5%; Pred. No. 0.015;
Matches 70; Conservative 52; Mismatches 11; Indels 93; Gaps 16;
Qy 46 NLEPF--LKRVD-----ADADPRQY-ADTVKALR-VRRITVGAQVP--AQLL 87
Db 158 NVTFSEIRIDFAGLTSLNELETKALSLRNYOSQSLKSIDRIHLLHLSESAFLLEIF 217
Qy 88 VGLRVLAYSRLEKLTLEDLKITCTMPPLPLEATGLALSSLRLLNNVSWATGRSW--LAEL 145
Db 218 ADILSSVRYLELRDTNLRQFS---PLPVDVSSPMKKLAERG-SVLTDESFNELLKL 272
Qy 146 QQWL-----KPG-----LKVLISIAQAHSPAF----- 166
Db 273 LRYILELSEVEFDCTNLGLGDFNPSSSDVVSLELKVETVTRIRLHLPQFVLYFDLSTVY 332
Qy 167 -----SYEQVRAF-----PALTSLDLSDNPGGLGERGLMAALCPHKFPATQN 207
Db 333 SLLEKVKRITVENSKEVFLVPCFSQHLKSLFELDLSENLMVEEYKNSACKGAWPSLQT 391
Qy 208 LALRNTGMET--PTGVCAALAAAGVQHSGLDLSHSLRATVNPSPAPRCMWSALNSLNS 265
Db 392 LVLSQNHLSRMQKTG---EILLTLKNTLSLDSN-----TFHPMPDSCQWPKRMFLNLS 444
Qy 266 FAGLEQVPGKLPKALRVLDLSCNPLN 291
Db 445 STGIRVVKTCIPQTLLEVLDVSNNNLD 470

Search completed: October 4, 2004, 16:54:51

Job time : 30 secs

283 LDLSNRLNRAPQP-DELPVDNLTLDGNPLVPGTALPHEGSMMS 327
||| ||| : : : : :
453 LDLHNNRIMSIPKQWTHLQALQELNVA NSL-----TDLPGGARSS 494

RESULT 12
PSKR DAUCA
ID PSKR DAUCA STANDARD; PRT; 1021 AA.
AC QBLPB4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Phytosulfokine receptor precursor (EC 2.7.1.37) (Phytosulfokine LRR
receptor kinase).
GN PSKR.

OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Apiales; Apiaceae; Apioidae; Scandiceae; Daucinae;
OC Daucus.
CN NCBI_TaxID=4039;
RX [1]
RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND GLYCOSYLATION.
EX MEDLINE=22025707; PubMed=12029134;
RA Matsubayashi Y., Ogawa M., Morita A., Sakagami Y.;
RT "An LRR receptor kinase involved in perception of a peptide plant
hormone, phytosulfokine.";
RL Science 296:1470-1472(2002).

CC -I- FUNCTION: Receptor with a serine/threonine-protein kinase
activity. Regulates, in response to phytosulfokine binding, a
signaling cascade involved in plant cell differentiation,
organogenesis and somatic embryogenesis.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane (By
similarity).
CC -I- TISSUE SPECIFICITY: Expressed ubiquitously in leaf, apical
meristem, hypocotyl and root.
CC -I- PTM: N-glycosylated.
CC -I- MISCELLANEOUS: A 36 amino-acid island is present in the 18th
leucine-rich repeat. An island domain has also been found among
the extra-cellular LRRs of the brassinosteroid receptor BRI1 and
has been shown to be critical for its function.
CC -I- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -I- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.

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EMBL: AB060167; BAC00995.1; --
DR InterPro; IPRO01611; LRR.
DR InterPro; IPRO07090; LRR_plant.
DR InterPro; IPRO00719; Prot_kinase.
DR InterPro; IPRO08271; Ser_thr_pkin_AS.
DR InterPro; IPRO02290; Ser_thr_pkinase.
DR InterPro; IPRO01245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 13.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHPRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Kinase; Serine/threonine-protein kinase; Receptor;
ATP-binding; Repeat; Leucine-rich repeat; Signal; Transmembrane;
KW Glycoprotein.


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Db 227 PREISKHLAKLDSYNPLKCSIPKSGFGLHNLILNLSVAELIGIPPELGNCKSLKS 286
Qy 283 LDLSNCRNLRAPODELPEV-----DNLTIDGNPFPLVPG 316
Db 287 LMLSFNLS-GPLPLESEIPLTFSAERNQLSGSLPWWGKVKVLSLLANNRF---S 342
Qy 317 TALPHE-----GSMNGSVVP--ACARSTL-SVGVSGLV 347
Db 343 GEIPHEIEDCPMLKHLSLASNLGSGSIPRELCSGSLAIDLGNLL 389

RESULT 11
TLR1 MOUSE
ID TLR1 MOUSE STANDARD; PRT; 795 AA.
AC Q9BQ1; Q9EPW5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like)
DE (TLR1).
GN TLR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Macrophage;
RX MEDLINE=20558581; PubMed=11095740;
RA Ozinsky A., Underhill D.M., Fontenot J.D., Hajjar A.M., Smith K.D.,
RA Wilson C.B., Schroeder L., Aderem A.;
RT "The repertoire for pattern recognition of pathogens by the innate
RT immune system is defined by cooperation between Toll-like
RT receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 97:13766-13771(2000).
[2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=20571875; PubMed=11123271;
RA Hajjar A.M., O'Mahony D.S., Ozinsky A., Underhill D.M., Aderem A.,
RA Klebanoff S.J., Wilson C.B.;
RT "Functional interactions between Toll-like receptor (TLR) 2 and TLR1
RT or TLR6 in response to phenol-soluble modulins."
RL J. Immunol. 166:15-19(2001).
[3]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RA Thomson D.P., Campbell C.C., Liew F.Y., Xu D.;
RT "Cloning of Mus musculus Toll-like receptor 1."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Participates in the innate immune response to microbial
CC agents. Cooperates with TLR2 and modulates the response to
CC microbial constituents. Acts via MyD88 and TRAF6, leading to NF-
CC kappa-B activation, cytokine secretion and the inflammatory
CC response (By similarity).
CC -!- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC -!- SIMILARITY: Contains 1 TIR domain.
CC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
CC
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CC
CC EMBL; AY009154; ANG37302.1; --

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DR EMBL; AF316985; AAC35062.1; --
DR HSP; O60603; IPYW.
DR MGD; MGI:1341295; Tlr1.
DR GO; GO:0016020; C:membrane; NAS.
DR GO; GO:0045335; C:phagocytic vesicle; NAS.
DR GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR GO; GO:0004988; F:transmembrane receptor activity; NAS.
DR GO; GO:0042497; F:triacylated lipoprotein binding; NAS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.
DR GO; GO:0042116; P:perception of triacylated bacterial lipopro. . ; NAS.
DR GO; GO:0042495; P:macrophage activation; NAS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . ; IMP.
DR GO; GO:0042535; P:positive regulation of tumor necrosis facto. . ; IMP.
DR InterPro; IPR004075; ILL_receptor1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNKIRIF.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SMO0082; LRRCT; 1.
DR SMART; SMO0255; TIR; 1.
DR PROSITE; PS01014; TIR; 1.
DR Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 25
FT CHAIN 26 795
FT DOMAIN 26 582
FT TRANSMEM 583 603
FT DOMAIN 604 795
FT REPEAT 46 70
FT REPEAT 71 94
FT REPEAT 96 116
FT REPEAT 117 140
FT REPEAT 140 140
FT REPEAT 374 397
FT REPEAT 400 427
FT REPEAT 447 470
FT REPEAT 471 494
FT REPEAT 496 515
FT REPEAT 515 515
FT DOMAIN 638 782
FT CARBOHYD 38 38
FT CARBOHYD 59 59
FT CARBOHYD 88 88
FT CARBOHYD 140 140
FT CARBOHYD 166 166
FT CARBOHYD 251 251
FT CARBOHYD 296 296
FT CARBOHYD 333 333
FT CARBOHYD 432 432
FT CONFLICT 88 88
SQ SEQUENCE 795 AA; 90672 MW; 855356429872D232 CRC64;
Query Match 7.5%; Score 138; DB 1; Length 795;
Best Local Similarity 21.3%; Pred. No. 0.0038;
Matches 61; Conservative 50; Mismatches 113; Indels 62; Gaps 9;
Qy 68 KALRVRLTVGAQVPAQLLVGLARVLAYSRLKLTLEDLKITGTMPLEATGLALSS 127
Db 245 KNLKLSNLTLNNVETTNNSFINLIQIVWHTPVKYSINVKLQGL-----A 291
Qy 128 LRLNVSWATGSRWLAELQWLKPLKVLSTAQHSFAFSYEQVRAFPALTSLDSDNPG 187
Db 292 FRMFNYS-----DTSLKALSIHQVVDVFSFPQSIIYSIFANMNI-QNFT 335
Qy 188 LGERGLMAALCP-----HKFPAIOMLALNTGMTPTGCA 223
Db 336 MSGTHVMHMLCPSQVSQVPLHVDFDTNLTDMVFDRCNLVRLKTLKSNQKNLENIL 395
Qy 224 ALAAGVQPHSLDLSHNSLRATVNPSPAPRCWSSALNSLNLSFAGLE-QVFKGLFAKLRV 282
Db 396 T-SAKWTSLOKLDLSQNSLR--YSDGGIPCAWTQSLLLVLSNMLTGSVFRCLPPKVKV 452

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RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,
 RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N., J.,
 RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,
 RA Martensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Voickaert G., Wambutt R., Dueterhoeft A., Stiekema W., Pohl T.,
 RA Entian K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
 RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
 RA Ransperger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R.,
 RA Weitzenecker T., Bothe G., Rose M., Hauf J., Berner S., Hempel S.,
 RA Feldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
 RA Schueller C., Zaccaria P., Meves H.-W., Bevan M., Franz P.F.,
 RA "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 RA thaliana",
 RL Nature 408:923-926(2000).
 CC -!- FUNCTION: Receptor with a serine/threonine-protein kinase
 CC activity required for the specification of the correct number of
 CC male archesporial initials and for the subsequent specification of
 CC tapetal and middle cell layer identities. In seeds, required for
 CC enhancing cell size and the rate of embryonic development.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
 CC -!- TISSUE SPECIFICITY: Present in young buds, open flowers and
 CC siliques but absent from mature leaves and roots. Strongly
 CC expressed in the young organ primordia, and as the anthers and
 CC ovules developed, became focused in the microsporangia and in the
 CC distal and chalazal regions of the ovule. In cv. Landsberg erecta,
 CC only expressed in the anthers of young floral buds.
 CC -!- DEVELOPMENTAL STAGE: Expressed during the differentiation of
 CC microsporocytes and tapetal cells. Also expressed in the meiocytes
 CC and young pollen grains until pollen mitosis II.
 CC -!- PTM: Autophosphorylates in vitro.
 CC -!- MISCELLANEOUS: Some ecotypic variation may occur: in cv.
 CC Landsberg erecta, meiocytes of a null mutant fail to undergo
 CC cytokinesis while in cv. C24, cytokinesis clearly takes place,
 CC with the mutant meiocytes degenerating shortly after the tetrad
 CC stage.
 CC -!- MISCELLANEOUS: In cv. C24, the gene is expressed in the young
 CC ovular primordia, but the protein is not present in these organs.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC -!- SIMILARITY: Contains 29 leucine-rich (LRR) repeats.
 CC -----
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 CC -----
 DR EMBL; AJ496433; CAD2912.1; -
 DR EMBL; AJ488154; CAD32463.1; -
 DR EMBL; AL163652; CAB87284.1; -
 DR PIR; T48499; T48499.
 DR GeneOnline; 181167; -
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00560; LRR; 19.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR Transferase; Kinase; Serine/threonine-protein kinase; Receptor;
 KW ATP-binding; Repeat; Signal; Transmembrane; Leucine-rich repeat;

KW Phosphorylation; Meiosis.
 FT SIGNAL 1 18
 FT CHAIN 19 1192

POTENTIAL.
 LEUCINE-RICH REPEAT RECEPTOR PROTEIN
 KINASE EXS.

FT REPEAT 64 87
 FT REPEAT 88 112
 FT REPEAT 114 135
 FT REPEAT 136 160
 FT REPEAT 162 185
 FT REPEAT 187 209
 FT REPEAT 233 256
 FT REPEAT 258 280
 FT REPEAT 281 305
 FT REPEAT 307 327
 FT REPEAT 328 351
 FT REPEAT 352 376
 FT REPEAT 378 399
 FT REPEAT 400 424
 FT REPEAT 426 447
 FT REPEAT 449 470
 FT REPEAT 471 495
 FT REPEAT 497 518
 FT REPEAT 519 543
 FT REPEAT 545 569
 FT REPEAT 579 602
 FT REPEAT 603 626
 FT REPEAT 627 651
 FT REPEAT 653 674
 FT REPEAT 676 698
 FT REPEAT 699 723
 FT REPEAT 725 746
 FT REPEAT 747 770
 FT REPEAT 771 796
 FT TRANSMEM 828 848
 FT DOMAIN 917 1192
 FT NP BIND 923 931
 FT BINDING 945 945
 FT ACT SITE 1043 1043
 FT MUTAGEN 4 4
 FT MUTAGEN 104 104
 FT MUTAGEN 1185 1185
 FT MUTAGEN 131 132
 FT CONFLICT 138 138
 FT CONFLICT 155 155
 FT CONFLICT 209 209
 FT CONFLICT 258 258
 FT CONFLICT 273 273
 FT CONFLICT 325 325
 FT CONFLICT 347 347
 FT CONFLICT 572 572
 FT CONFLICT 852 852
 FT CONFLICT 866 866
 FT CONFLICT 1075 1075
 SQ SEQUENCE 1192 AA; 129799 MW; D02C8B8FF6B09F7D CRC64;

Query Match 7.7%; Score 142; DB 1; Length 1192;
 Best Local Similarity 23.9%; Pred. No. 0.0031;
 Matches 83; Conservative 48; Mismatches 116; Indels 100; Gaps 14;

QY 77 VGAQVPAQLLVGAL--RVLAYSRKLTLEDKLTGTMP-----LPLEATGLALS 126
 Db 67 VNSLSLPSLSLRGQIPKEISSLNKRLCLAGNQFSKIPETIWNKHLQTLDSGNLSL 126
 QY 127 SLRLRVSWATGRSWLAELQQWLKPGKVLISIAQAHSFASFEQVRAFPALTSLDSDNP 186
 Db 127 GLLP-----LISELPQLLYLDLSDNHSSLPSPFFI----SLPALSSLDVSNNS 173
 QY 187 GLGERGLMAALCPHKFPAIONLALRNTGMEPTPTG-----VCAALAAA-----GVQ 231
 Db 174 LSQE-----IPPEIGKLSNLSNLYMGNLSFGSQIPSEIGNISLLKNFAAPSCFFNGPL 226
 QY 232 PH-----SLDLSHNSLRATVNPSPAPRCMSSALNSLNSLFAGLEQVPKGLPAKLVR 282

CC -1- SIMILARITY: Contains 1 TIR domain.
CC -1- SIMILARITY: Contains 8 leucine-rich (LRR) repeats.
CC -----
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CC -----
DR EMBL; U88540; AAC34137.1; -;
DR EMBL; D13637; BAA02801.1; -;
DR EMBL; AL050262; CAB43364.1; -;
DR PIR; T08664; T08664.
DR PDB; 1FYW; 22-NOV-00.
DR Genew; HGNC:11847; TLR1.
DR MIM; 601194; -;
DR GO; GO:0016020; C:membrane; NAS.
DR GO; GO:0045335; C:phagocytic vesicle; ISS.
DR GO; GO:0003793; F:defense/immunity protein activity; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; NAS.
DR GO; GO:0042497; F:triacylated lipoprotein binding; ISS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0042116; P:macrophage activation; NAS.
DR GO; GO:0042495; P:perception of triacylated bacterial lipopro. .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. .; ISS.
DR GO; GO:0042535; P:positive regulation of tumor necrosis facto. .; ISS.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR001611; LRR_1.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNMRIF.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS01014; TIR; 1.
KW Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein;
KW 3D-structure.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 786 TOLL-LIKE RECEPTOR 1.
FT DOMAIN 23 580 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 581 601 POTENTIAL.
FT DOMAIN 602 786 CYTOPLASMIC (POTENTIAL).
FT REPEAT 68 91 LRR 1.
FT REPEAT 93 113 LRR 2.
FT REPEAT 114 137 LRR 3.
FT REPEAT 139 164 LRR 4.
FT REPEAT 371 395 LRR 5.
FT REPEAT 397 423 LRR 6.
FT REPEAT 444 467 LRR 7.
FT REPEAT 469 491 LRR 8.
FT DOMAIN 635 779 TIR.
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 429 429 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 578 578 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 80 80 R -> T (IN REF. 2).
FT CONFLICT 182 182 E -> G (IN REF. 3).
FT CONFLICT 228 228 N -> S (IN REF. 3).
FT CONFLICT 248 248 S -> N (IN REF. 2).
FT CONFLICT 276 276 F -> S (IN REF. 3).
FT CONFLICT 602 602 I -> S (IN REF. 2).
SQ SEQUENCE 786 AA; 90290 MW; 1408C60FB5847F58 CRC64;

Query Match 7.8%; Score 144; DB 1; Length 786;
Best Local Similarity 24.9%; Pred. No. 0.0013;

Matches 71; Conservative 39; Mismatches 115; Indels 60; Gaps 10;
QY 94 LAYSRKLTLEDLKLTGMPPLPLEATGLAISLRNVSWATGRSLAELQ-----146
DB 216 LELSNIK-CVLEDNKCSYFLSILAKLTNPKLSLNNIE-TTWSFKILQLVWHTTV 273
QY 147 -----QWLKPGKLVLSIAQHPAFSYEQVRAPPALTSLDSDNPG 187
DB 274 WYFSINVKLQGLDFRDPDYSCTSLKALSIHQWSDVFGFPOSYIYEFNSNNIKFTV 333
QY 188 LGRGLMAALCPHKFPAIONLARN-----TGMET-----PTGVCAA 224
DB 334 SGTR-VVHMLCPKISPFHLHDFSNLLTDTVFENCCHLTELTLIQMNLKELSKIAE 392
QY 225 LAAGVQPHSLDLSHSLRATVNPSPROMWSALNSLNSFAGL-EQVPGKLPKURVL 283
DB 393 MTTQMKSLQQLDISQNSV--SYDEKKGDCSWTKSLJSLNWSNLLTITFRCLPPRIKVL 450
QY 284 DLSCNRLNRP-OPDELPEVDNLTLDGNPFLVPGTALPHEGSMNS 327
DB 451 DLHSNKIKSPKQVKLEALQELNVAFNSL----TDLPGCGSFSS 491
RESULT 10
EXS_ARATH
ID EXS_ARATH STANDARD; PRT; 1192 AA.
AC Q9LYNB; Q8GSM5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leucine-rich repeat receptor protein kinase EXS precursor
DE (EC 2.7.1.37) (Extra sporogenous cells protein) (EXCESS
DE MICROSPOROCTESI protein)
DE EXS OR ESP OR EMS1 OR ATSG07280 OR T28J14.220.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, DEVELOPMENTAL STAGE, AND
RP MUTANTS EXS-1 AND GNE2/EXS-2.
RC STRAIN=cv. C24; TISSUE=Flower;
RX MEDLINE=22288931; PubMed=12401166;
RA Canales C.S., Bhatt A.M., Scott R.J., Dickinson H.G.;
RT "EXS, a putative lrr receptor kinase, regulates male germline cell
RT number and tapetal identity and promotes seed development in
RT arabidopsis complex ancf in the promoter of a penicillin biosynthesis
RT gene.";
RL Curr. Biol. 12:1718-1727(2002).
RN [2]
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, DEVELOPMENTAL STAGE, AND
RP MUTANTS REV.1 AND REV.2.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=22148765; PubMed=12154130;
RA Zhao D.-Z., Wang G.-F., Speal B., Ma H.;
RT "The EXCESS MICROSPOROCTESI gene encodes a putative leucine-rich
RT repeat receptor protein kinase that controls somatic and reproductive
RT cell fates in the Arabidopsis anther.";
RN Genes Dev. 16:2021-2031(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016721; PubMed=11130714;
RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Belter E., Cordum H., Cordes M., Courtney W., Dante M.,

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EMBL; AY045573; AAK91868.1; -
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 4.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNK1RIF.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS0104; TIR; 1.
DR Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 18
FT CHAIN 19 784
FT DOMAIN 19 587
FT TRANSMEM 588 608
FT DOMAIN 609 784
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FT REPEAT 412 436
FT REPEAT 438 456
FT REPEAT 457 476
FT REPEAT 477 499
FT REPEAT 501 521
FT REPEAT 521 544
FT DOMAIN 544 784
FT CARBOHYD 114 114
FT CARBOHYD 199 199
FT CARBOHYD 414 414
FT CARBOHYD 442 442
SQ SEQUENCE 784 AA; 89987 MW; 3386E36DB32CAB3E CRC64;

Query Match
Best Local Similarity 21.5%; Score 144; DB 1; Length 784;
Matches 83; Conservative 62; Mismatches 141; Indels 100; Gaps 16;

QY 4 EPCLEDDPRFCVNFSEFPQDWEAFQCVSAVEIHAGGLNLEFP-----LKR 54
Db 177 ELEIDASLQSY-----EPKSLGIQNVSHLILHMKQHLLLEIFVDLTSSVECLELR 230
QY 55 DADADPROVAD---TVKALRVERLTVGAAQVPAQLLVGLARVLA-YSLKELTLEDLKI 109
Db 231 DTDLDTFHSELSGTGNSL-INKFTFRNVKTTDESLFQVMKLSQISGLLEFPDCTL 289
QY 110 TGMPLPLEATGLALSLRLNRVSWATGRSLWALQQLKPG-LKVLSTQAQHSFAF-- 166
Db 290 NG-----VDFRGSDDNDVIDPGKVETVIRRLHIQFYVS 324
QY 167 -----SYEQYRAF--PALTS-----LQSDNPGLGGERGLMAALCP 199
Db 325 FNDLSTLYPLTRVRKVTIVNSKFLVPLCLSRHLKSLRYLDLSENL-MVEEYLNKNSACE 383
QY 200 HKFFAIONIALRNTGNETPTGVCAALAAAG-----VQPHSLDLSHSLRATVNPSPAPRC 253
Db 384 DAWPSIQTLILRQNL-----ASLGKGTGELLTKLNTLNDISKV-----TFHYMPETC 432

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QY 254 MWSSALNSINLSFAGLEQVPKCLPAKLVLDLSCNLRNAPQDPDELPEVDNLTLDGNPFL 313
Db 433 QMPEKKNYLSSTRIHSVTGCIPTKLTLEILDSNNNLNLFSL--NLPOLKELYISRNKILM 490
QY 314 VPGTALPHEGSMNSGVWPACARSTLS 339
Db 491 ---TLPDASLLPMLLVLKISNTIT 512

RESULT 9
TLR1 HUMAN
ID TLR1 HUMAN STANDARD; PRT; 786 AA.
AC Q15399; O15452; Q9UG90;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like) (TIL).
GN TLR1 OR KIAA0012.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN 1
RN PP SEQUENCE FROM N.A.
RC TISSUE=Erythrocytes;
RC MEDLINE=96118556; PubMed=9435236;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila Toll.";
RT Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
RN 2
RN PP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RC MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1.";
RT DNA Res. 1:27-35(1994).
RN 3
RN PP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RC MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansoerger W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
RA Mewes H.-W., Othenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RT Genome Res. 11:422-435(2001).
RN 4
RN PP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF TIR DOMAIN.
RX MEDLINE=20531768; PubMed=11081518;
RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/interleukin-1
RT receptor domains.";
RL Nature 408:111-115(2000).
CC -!- FUNCTION: Participates in the innate immune response to microbial
CC agents. Cooperates with TLR2 and modulates the response to
CC microbial constituents. Acts via MyD88 and TRAF6, leading to NF-
CC kappa-B activation, cytokine secretion and the inflammatory
CC response (By similarity).
CC -!- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes (By similarity).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in spleen, ovary,
CC peripheral blood leukocytes, thymus and small intestine.
CC -!- SIMILARITY: Belongs to the Toll-like receptor family.

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soluble tuberculosis factor (STF), phenol-soluble modulin (PSM) and B.burgdorferi outer surface protein A lipoprotein (OspA-L) cooperatively with TLR6.

-!- SUBUNIT: Binds LY96 and TLR6 via the extracellular domain. Binds MYD88 via their respective TIR domains.

-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-!- TISSUE SPECIFICITY: Highly expressed in peripheral blood leukocytes, in particular in monocytes, in bone marrow, lymph node and in spleen. Also detected in lung and in fetal liver. Levels are low in other tissues.

-!- PM: N-glycosylated (By similarity).

-!- SIMILARITY: Belongs to the Toll-like receptor family.

-!- SIMILARITY: Contains 1 TIR domain.

-!- SIMILARITY: Contains 14 leucine-rich (LRR) repeats.

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EMBL: AF051152; AAC34377.1; --
 EMBL: U89878; AAC34133.1; --
 EMBL: BC033756; AAH33756.1; --
 PDB: 1FYW; 22-NOV-00.
 PDB: 1FYX; 22-NOV-00.
 Genew: HGNC:11848; TLR2.
 MIM: 603028; --
 GO: GO:0005515; F:protein binding; ISS.
 InterPro: IPR004075; IL1_receptor1.
 InterPro: IPR001611; LRR.
 InterPro: IPR000483; LRR_Cterm.
 InterPro: IPR003591; LRR typ.
 InterPro: IPR00157; TIR.
 Pfam: PF00560; LRR; 4.
 Pfam: PF01463; LRRCT; 1.
 Pfam: PF01582; TIR; 1.
 PRINTS: PR01537; INTRLNRI1F.
 PRINTS: PR00019; LEURICHRPT.
 SMART: SM00369; LRR_TYP; 2.
 SMART: SM00082; LRRCT; 1.
 SMART: SM00255; TIR; 1.
 PROSITE: PS0104; TIR; 1.
 Receptor; Immune response; Inflammatory response; Signal;
 Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein;
 3D-structure.

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 SIGNAL
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 FT DOMAIN 19 588
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 FT DOMAIN 610 784
 FT REPEAT 51 74
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DR SMART; SMO0262; GEL; 6.
 DR SMART; SMO0369; LRR TYP; 1.
 KW Developmental protein; Repeat; Leucine-rich repeat; Actin-binding;
 KW Polymorphism.
 FT REPEAT 4 28 LRR 1.
 FT REPEAT 29 51 LRR 2.
 FT REPEAT 52 74 LRR 3.
 FT REPEAT 75 99 LRR 4.
 FT REPEAT 100 122 LRR 5.
 FT REPEAT 124 145 LRR 6.
 FT REPEAT 147 169 LRR 7.
 FT REPEAT 171 192 LRR 8.
 FT REPEAT 218 241 LRR 9.
 FT REPEAT 243 264 LRR 10.
 FT REPEAT 265 287 LRR 11.
 FT REPEAT 289 312 LRR 12.
 FT REPEAT 313 335 LRR 13.
 FT REPEAT 336 358 LRR 14.
 FT REPEAT 360 381 LRR 15.
 FT REPEAT 499 557 GELSOLIN-LIKE 1.
 FT REPEAT 746 789 GELSOLIN-LIKE 2.
 FT REPEAT 1064 1102 GELSOLIN-LIKE 3.
 FT REPEAT 1165 1206 GELSOLIN-LIKE 4.
 FT VARIANT 601 601 G -> S.
 FT CONFLICT 1067 1070 STFC -> HYFS (IN REF. 5).
 FT CONFLICT 1068 1068 T -> A (IN REF. 2).
 SQ SEQUENCE 1256 AA; 143681 MW; CF0056FAA88DB92 CRC64;

Query Match 8.2%; Score 150.5; DB 1; Length 1256;
 Best Local Similarity 23.0%; Fred. No. 0.00072;
 Matches 92; Conservative 48; Mismatches 103; Indels 157; Gaps 18;

45 LNPFLPKRVADADAD--PROVADTVKAL-RVRRLTVG---AAQVPAQL----- 86
 1 MSVLVFRGVDFDKNDFSAFPPSMRQMSRVQMLTDLTQTLAEIPPELGHLOKLEHJSLN 60
 87 -----LVGALRVLAYSRLKELTDLKITGTPPL--PLEATGLALSSLRNRVSWATG 138
 61 HNRLEKIFGELTSLCLSLDLRHNLKNSGIPPELFLHELTTLTDLSHNKLKEVPGLE 120
 139 RSWLAELQWLKGLKVLSTAQAH-----SPAP-----SYQVRAFP----- 176
 121 RA-----KRLIVNLNNSNQIESIPTPLFTHITDLLFLDLSHNRLETLPQTRRLI 170
 177 -LTSLDLSDNPGGLGERGMAALCPHKPAIQNLAL-----RNTGMEPTPGVCAALAAAG 229
 171 NLKTLDSHNP-----LELFQRLQPSLQSLVLMKSGTQRTLLNFPPTSIDSLANLC- 222
 230 VQPHSLDLSHNSLRATVNPSPACWMS-----SALNSLNLS 265
 223 -----ELDLSHNSL-----PKLPDCVYVNVTVLRLNLSDELTELTAGVELWQRLSLSNLS 273
 266 -----FAG-----LSQVPKGL- 276
 274 RNQLVALPAALCKLPKRLRLVNDKLNLFEGIPSGIGKLGALVFSAAANNLLEWVPRGLC 333
 277 -PAKLRLVLDLSCNLRNAPQDELPE-VDNLTLDGNPFV 314
 334 RCQALKQLNLSNRLITLPAIHLEGLDQLDRNPELV 373

RESULT 7
 TLR2 HUMAN
 ID TLR2 HUMAN STANDARD; PRT; 784 AA.
 AC O60603; O15454;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Toll-like receptor 2 precursor (Toll/interleukin 1 receptor-like protein 4).
 GN TLR2 OR TIL4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte, and Prostate;
 RX MEDLINE=98261424; PubMed=9596645;
 RA Chaudhary P.M., Ferguson C., Nguyen V., Nguyen O., Massa H.F., Eby M.,
 RA Jasmin A., Trask B.J., Hood L., Nelson P.S.;
 RT "Cloning and characterization of two Toll/interleukin-1 receptor-like
 RT genes TIL3 and TIL4: evidence for a multi-gene receptor family in
 RT humans.";
 RL Blood 91:4020-4027(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98118556; PubMed=9435236;
 RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
 RT "A family of human receptors structurally related to Drosophila
 RT Toll.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
 RN [3]
 RP SEQUENCE FROM N.A., AND RESPONSE TO LIPOPOLYSACCHARIDE.
 RC TISSUE=Fetal lung;
 RX MEDLINE=98421677; PubMed=9751057;
 RA Yang R.-B., Mark M.R., Gray A., Huang A., Xie M.H., Zhang M.,
 RA Goddard A., Wood W.I., Gurney A.L., Godowski P.J.;
 RT "Toll-like receptor-2 mediates lipopolysaccharide-induced cellular
 RT signalling.";
 RL Nature 395:284-288(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP RESPONSE TO BACTERIAL LIPOPROTEINS.
 RX MEDLINE=99357867; PubMed=10426996;
 RA Aliprantis A.O., Yang R.-B., Mark M.R., Suggett S., Devaux B.,
 RA Radolf J.D., Kimpel G.R., Godowski P.J., Zychlinsky A.;
 RT "Cell activation and apoptosis by bacterial lipoproteins through
 RT Toll-like receptor-2.";
 RL Science 285:736-739(1999).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF TIR DOMAIN, AND MUTAGENESIS.
 RX MEDLINE=20531768; PubMed=11081518;
 RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
 RT "Structural basis for signal transduction by the Toll/interleukin-1
 RT receptor domains.";
 RL Nature 408:111-115(2000).
 CC - FUNCTION: Cooperates with LY96 to mediate the innate immune
 CC response to bacterial lipoproteins and other microbial cell wall
 CC components. Acts via MyD88 and TRAF6, leading to NF-kappa-B
 CC activation, cytokine secretion and the inflammatory response. May
 CC also promote apoptosis in response to lipopeptides. Recognizes
 CC mycoplasma macrophage-activating lipopeptide-2kD (MALP-2),

Db 370 F 370

RESULT 6

FLII DROME STANDARD; PRT; 1256 AA.

AC Q24020: Q24089; Q9VRH0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Flightless-I protein.

GN FLII OR CGI484.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Oregon-R; TISSUE=Embryo;

RX MEDLINE=94068608; PubMed=8248259;

RA Campbell H.D., Schimanski T., Claudianos C., Oszarac N.,

RA Kasprzak A.B., Cotwell J.N., Young I.G., de Couet H.G., Miklos G.L.G.;

RT "The Drosophila melanogaster flightless-I gene involved in

RT gastrulation and muscle degeneration encodes gelsolin-like and

RT leucine-rich repeat domains and is conserved in Caenorhabditis elegans

and humans.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:11386-11390(1993).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANT SER-601.

RC STRAIN=Canton-S;

RX MEDLINE=96129280; PubMed=8582612;

RA de Couet H.G., Fong K.S.K., Weeds A.G., McLaughlin P.J.,

RA Miklos G.L.G.;

RT "Molecular and mutational analysis of a gelsolin-family member encoded

RT by the flightless I gene of Drosophila melanogaster.";

RL Genetics 141:1049-1059(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Canton-S;

RX MEDLINE=98188272; PubMed=9520435;

RA Maleszka R., de Couet H.G., Miklos G.L.G.;

RT "Data transferability from model organisms to human beings: insights

RT from the functional genomics of the flightless region of Drosophila.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3731-3736(1998).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley; TISSUE=Embryo;

RX MEDLINE=20196012; PubMed=10731138;

RA Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,

RA Stapleton M., Harvey D.A.;

RT "A Drosophila complementary DNA resource.";

RL Science 287:2222-2224(2000).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

RA Bellow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunderson R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RN [6]

RP REVISIONS.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083.22(2002).

CC -!- FUNCTION: May play a key role in embryonic cellularization by

interacting with both the cytoskeleton and other cellular

components. Alternatively, it may play a structural role in

indirect flight muscle. Vital for embryonic development.

CC -!- TISSUE SPECIFICITY: Found in ovaries, larval fat bodies, brain and

adult thorax.

CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.

CC -!- DOMAIN: CONSISTS OF A LEUCINE-RICH AMINO TERMINAL HALF, WHICH IS

LIKELY TO BE INVOLVED IN PROTEIN-PROTEIN INTERACTION, AND A

CARBOXYTERMINAL HALF WHICH HAS HIGH SEQUENCE SIMILARITY TO

GELSOLIN AND IS THEREFORE LIKELY TO BE INVOLVED IN ACTIN-BINDING.

CC -!- SIMILARITY: Belongs to the villin/gelsolin family.

CC -!- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.

CC -!- SIMILARITY: Contains 4 gelsolin-like repeats.

CC -----

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CC -----

CC EMBL; U01182; AAC03566.1; -

CC EMBL; AF017777; AAC28407.1; -

CC EMBL; AF132184; AAD34772.1; -

CC EMBL; AE003568; AAF50830.2; -

CC F01; S60461; S60461.

CC HSP; P02640; 2VIL.

CC FlyBase; FBgn0000709; flil.

CC InterPro; IPR007122; Gelsolin.

CC InterPro; IPR007123; Gelsolin.

CC InterPro; IPR001611; LRR.

CC InterPro; IPR003591; LRR_type.

CC Pfam; PF00626; Gelsolin; 5.

CC Pfam; PF00560; LRR; 12.

CC PRINTS; PR00597; GELSOLIN.

CC PRINTS; PR00019; LEURICHRPT.

[3]
RN
RP
RX
RA
RT
RT
RT
RL

SEQUENCE FROM N.A.
MEDLINE=90293480; PubMed=1694207;
Ferrero E, Hsieh C.L., Francke U., Goyert S.M.;
"CD14 is a member of the family of leucine-rich proteins and is
encoded by a gene syntenic with multiple receptor genes."; *J. Immunol.* 145:331-336(1990).

ID_	CD14_MOUSE
ID_	CD14_MOUSE
AC	P10810; STANDARD; PRT; 366 AA.
DT	01-JUL-1989 (Rel. 11, Created)
DT	01-JUL-1989 (Rel. 11, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein).
DE	leucine-rich glycoprotein).
GN	CD14.
GN	GN

SEQUENCE	366 AA;	39203 MW;	57C4492EC7EA3AA1	CRC64;
(Potential).				

Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J., Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[7]
 RN SEQUENCE OF 1-125 FROM N.A.
 RP TISSUE=Glioblastoma;
 RC Deininger M.H., Meyermaun R., Schluesener H.J.;
 RA Expression and secretion of CD14 in glial neoplasms of the brain.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL [8]
 RN SEQUENCE OF 362-367.
 RP MEDLINE=89384684; PubMed=2779588;
 RX Bazil V., Baudys M., Hilgert I., Stefanova I., Low M.G., Zbrozek J., Horejsi V.;
 RA "Structural relationship between the soluble and membrane-bound forms of human monocyte surface glycoprotein CD14.";
 RT Mol. Immunol. 26:657-662(1989).
 RL CC -!- FUNCTION: Cooperates with MD-2 and TLR4 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response. Up-regulates cell surface molecules, including adhesion molecules.
 CC CC -!- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, MD-2 and TLR4.
 CC CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC CC -!- TISSUE SPECIFICITY: Expressed strongly on the surface of monocytes and weakly on the surface of granulocytes; also expressed by most tissue macrophages.
 CC CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
 CC CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD14 entry;
 CC CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd14.htm".
 CC CC -----
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 CC CC -----
 DR EMBL; X06882; CAA29999.1; -;
 DR EMBL; X13334; CAA31711.1; -;
 DR EMBL; M86511; AAA51930.1; -;
 DR EMBL; AF097942; AAC81816.1; -;
 DR EMBL; BC010507; AAL10507.1; -;
 DR EMBL; AY044269; AAL02401.1; -;
 DR PIR; A27637; TDH0M4.
 DR Genew; HGNC:1628; CD14.
 DR MIM; 158120; -;
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0016019; P:peptidoglycan recognition activity; TAS.
 DR GO; GO:0006915; P:apoptosis; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 DR GO; GO:0006909; P:phagocytosis; TAS.
 DR InterPro; IPR001611; LRR.
 DR Pfam; PF00560; LRR; 2.
 DR Immune response; Inflammatory response; Signal; GPI-anchor; Repeat;
 KW Leucine-rich repeat; Glycoprotein; Antigen; Lipoprotein.

FT	SIGNAL	1	19	CD14 DIFFERENTIATION ANTIGEN.
FT CHAIN	20	375	CD14 DIFFERENTIATION ANTIGEN, URINARY	
FT CHAIN	20	367	FORM.	
FT	20	345	MONOCYTE DIFFERENTIATION ANTIGEN CD14.	
FT	20	345	REMOVED IN MATURE FORM (POTENTIAL).	
FT PROPEP	346	375	LRR 1.	
FT REPEAT	115	139	LRR 2.	
FT REPEAT	193	213	LRR 3.	
FT REPEAT	221	243	LRR 4.	
FT REPEAT	246	276	LRR 5.	
FT REPEAT	275	292	LRR 6.	
FT REPEAT	297	320	LRR 7.	
FT REPEAT	322	340	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	37	37	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	282	282	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	323	323	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT LIPID	345	345	GPI-anchor amidated asparagine (Potential).	
FT	77	77	A -> G (IN REF. 3).	
FT CONFLICT	187	187	C -> Y (IN REF. 1 AND 2).	
FT CONFLICT	303	303	D -> E (IN REF. 5).	
FT CONFLICT	303	303	Mismatches 1; Indels 0; Gaps 0;	
SQ SEQUENCE	375 AA;	40076 MW;	1746CDB41F394F8D CRC64;	
Query Match	99.5%;	Score 1831;	DB 1; Length 375;	
Best Local Similarity	99.7%;	Pred. No. 5.5e-137;		
Matches 355;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;	
QY 1	TTPEPCLEDDDEFRVCNCFSEPOQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP	60		
Db 20	TTPEPCLEDDDEFRVCNCFSEPOQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP	79		
QY 61	ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPLEA	120		
Db 80	ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPLEA	139		
QY 121	TGLALSRLRNYSWATGRSWLAELQWLKPLKVLISIAQHSFAFSVEQVRAFPALTS	180		
Db 140	TGLALSRLRNYSWATGRSWLAELQWLKPLKVLISIAQHSFAFSVEQVRAFPALTS	199		
QY 181	DLSDNPGIGERGLMAALCPHKFPAIQNALRLNTGNETPTTGVCAALAAAGVQPHSLDLSHN	240		
Db 200	DLSDNPGIGERGLMAALCPHKFPAIQNALRLNTGNETPTTGVCAALAAAGVQPHSLDLSHN	259		
QY 241	SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODPLP	300		
Db 260	SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODPLP	319		
QY 301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGTLVLLQGARGFA	356		
Db 320	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGTLVLLQGARGFA	375		
RESULT 2				
CD14_RABIT	STANDARD;	PRT;	372 AA.	
AC Q28680;				
DT 15-DEC-1998	(Rel. 37, Created)			
DT 15-DEC-1998	(Rel. 37, Last sequence update)			
DT 28-FEB-2003	(Rel. 41, Last annotation update)			
DE Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein).				
GN CD14.				
OS Oryctolagus cuniculus (Rabbit).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX NCBI_TaxID=9986;				
RN [1]				
RP SEQUENCE FROM N.A.				
RA MEDLINE=92268819; PubMed=1375269;				
RX Lee J.D., Kato K., Tobias P.S., Kirkland T.N., Ulevitch R.J.;				
RT "Transfection of CD14 into 702/3 cells dramatically enhances the sensitivity to complexes of lipopolysaccharide (LPS) and LPS binding				

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 25 Seconds
(without alignments)
741.479 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTPPCELDDDFRCVCFNS.....TLSSVSGTIVLLQARGFA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1831	99.5	375	1	CD14 HUMAN
2	1338.5	72.7	372	1	CD14_RABIT
3	1328.5	72.2	373	1	CD14_BOVIN
4	1136.5	61.8	366	1	CD14_MOUSE
5	1079	58.6	371	1	CD14_RAT
6	150.5	8.2	1256	1	FLII DROME
7	147.5	8.0	784	1	TLR2 HUMAN
8	144	7.8	784	1	TLR2_MACFA
9	144	7.8	786	1	TLR1 HUMAN
10	142	7.7	1192	1	EXS ARATH
11	138	7.5	795	1	TLR1_MOUSE
12	138	7.5	1021	1	PSKR DAUCA
13	135	7.3	781	1	TL22 CHICK
14	130.5	7.1	784	1	TLR2_CRIGR
15	130.5	7.1	784	1	TLR2_MOUSE
16	129.5	7.0	784	1	TLR2_BOVIN
17	126.5	6.9	1196	1	BR11 ARATH
18	124	6.7	662	1	GARP HUMAN
19	122.5	6.7	605	1	ALS PAPHA
20	120.5	6.5	1008	1	PSKR ARATH
21	120	6.5	793	1	TL21 CHICK
22	118.5	6.4	796	1	TLR6 HUMAN
23	118.5	6.4	811	1	TLR4 HUMAN
24	117	6.4	327	1	OPT CANFA
25	113.5	6.2	1024	1	POPC RALSO
26	113	6.1	481	1	NYX HUMAN
27	112.5	6.1	1032	1	TLR9 HUMAN
28	112.5	6.1	1032	1	TLR9_MOUSE
29	112	6.1	858	1	TLR5 HUMAN
30	112	6.1	1115	1	TBC2_CHIRE
31	111	6.0	828	1	LGR6_HUMAN
32	111	6.0	899	1	ZCH2_HUMAN
33	110	6.0	574	1	IPA4_SHIFL

ALIGNMENTS

RESULT 1
CD14 HUMAN
ID CD14 HUMAN STANDARD; Q96L99; Q9UN33; PRT; 375 AA.
AC P08571; Q96FR6; Q96L99; Q9UN33;
DT 01-AUG-1988 (Rel. 08, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein).
DE leucine-rich glycoprotein).
GN CD14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=88234022; PubMed=2453848;
RA Ferrero E., Goyert S.M.;
RT "Nucleotide sequence of the gene encoding the monocyte differentiation antigen, CD14.";
RL Nucleic Acids Res. 16:4173-4173(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258060; PubMed=3385210;
RA Haziot A., Chen S., Ferrero E., Low M.G., Silber R., Goyert S.M.;
RT "The monocyte differentiation antigen, CD14, is anchored to the cell membrane by a phosphatidylinositol linkage.";
RL J. Immunol. 141:547-552(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Macrophage;
MEDLINE=89287330; PubMed=2472171;
RA Setoguchi M., Nasu N., Yoshida S., Higuchi Y., Akizuki S., Yamamoto S.;
RT "Mouse and human CD14 (myeloid cell-specific leucine-rich glycoprotein) primary structure deduced from cDNA clones.";
RL Biochim. Biophys. Acta 1008:213-222(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89088540; PubMed=2462937;
RA Simmons D.L., Tan S., Tenen D.G., Nicholson-Weller A., Seed B.;
RT "Monocyte antigen CD14 is a phospholipid anchored membrane protein.";
RL Blood 73:284-289(1989).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Myelocytic leukemia;
RA Long J.Y., Xue Y.N., Sun L., Wang H.X.;
RT "Cloning and sequencing of human CD14 gene.";
RL Sheng Wu Huaxue Yu Shengwu Wuli Jinzhan 25:377-378(1998).
RN [6]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

34 109 5.9 605 1 ALS HUMAN P35858 homo sapien
35 107.5 5.8 361 1 CHAD_BOVIN Q27972 bos taurus
36 107.5 5.8 1061 1 NAI2_HUMAN P59046 homo sapien
37 107 5.8 1269 1 FLIH_HUMAN Q13045 homo sapien
38 106.5 5.8 331 1 PLIB_AGBEL O93233 agkistrodon
39 105.5 5.7 358 1 CHAD_RAT O70210 rattus norv
40 105.5 5.7 942 1 TMK1_ARATH P43298 arabidopsis
41 105.5 5.7 1504 1 SLIT_DROME P24014 drosophila
42 105 5.7 999 1 LUKS_ARATH P47735 arabidopsis
43 105 5.7 2224 1 FAS_HUMAN P12259 homo sapien
44 104.5 5.7 1315 1 CHAO_DROME P12024 drosophila
45 104 5.7 782 1 CHAO_TRICA P82963 tribolium c

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Db 105 YLQTLDSGNYFSGPLPDSLSNLTRLTLTVSGNSFSGSIPDS--VGMTV-----LEEL 157
QY 103 TLEDLKITGMPPLPLEATGLAULSSLR-----LRNVSWATGRSWLAELQWLKPGGLKVL 157
Db 158 VLDSNRLYGSIP-----ASFNGLSLKRLEIQLNNIS----- 189
QY 158 IQAHSFAFSYEQVRAFPALTS-----LDLSDNPGLGERGLMAALCPHKFP-AIQNAL 210
Db 190 -----GEPDLSLKNLYYLDASDN-----RISGRIPSELPESIVQISM 228
QY 211 RNTGMEPTGVCALAAAGVQPHS-----LDLSHNSLRATVNSAPRCMWS-SALN 260
Db 229 RNNLFQ-----GTPESFKLLNSLEVIDLSHNKLSGSI-----PSFIFTHQSLO 272
QY 261 SLNLSFAGLRQV-----PKGLPAKLRVLDLSCNR-LNRAPODEL-PEVDNLTLDGNPF 312
Db 273 QLTLSEFNGFTSLSEPYSPGLPSELISVDLSNNQILGALPLFMGLSPKLSALSLENNKF 332
QY 313 -----LVPGT-----ALPHEGSMNSGVVP-----ACARSTLSVGVSG----- 344
Db 333 FGMIPTQYVWKTVSPGSEFAGFQRLLLGGNPLFGVPGPLMAKPGSANVOLAGNCFSWC 392
QY 345 --TLVLLQG 351
Db 393 PATLFFCQG 401

RESULT 15
Q8NI00 PRELIMINARY; PRT; 586 AA.
AC Q8NI00;
BT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Toll-like receptor 2 (Fragment).
Q6 Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Yu W.B., Ma Y.Y.;
RT "Cloning and sequencing of extracellular domain and its N-Terminal and
RT C-Terminal fragments of Toll-like receptor 2.";
RL T1 4 Chun i Ta Hsueh Heueh Pao 23:0-0(2002).
DR EMBL; AF502291; AAM23001.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 3.
DR PRINTS; PF01463; LRRCT; 1.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Receptor.
FT NON TER.
SQ SEQUENCE 586 AA; 66281 MW; 6D676D752BE55C88 CRC64;

Query Match 8.0%; Score 147.5; DB 4; Length 586;
Best Local Similarity 22.3%; Pred. No. 0.0017;
Matches 82; Conservative 56; Mismatches 131; Indels 99; Gaps 17;
QY 4 EPCLEDDDEFCVCFSEFQPDWSEAFQCVSAVEIHHAGGLNLEPF-----LKR 54
Db 177 EELEIDASLQSY-----EPKSLKSTQNVSHLTHMKQHILLLEIFVDVTSSVECLELR 230
QY 55 DADADPRQYAD-----TVKALFRVRLTVGAQVPAQLLVGALRVL-AYSRLKELTLEDLKI 109

Db 231 DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLSFQVMKLNQISGLLELEFDDCTL 289
QY 110 TGTMPPLPLEATGLALSRLNRNVSWATGRSWLAELQWLKPG-LKVLSTIAQAHSAPF-- 166
Db 290 NG-----VGNFRASDNRVIDPGKVETLTTRRLHIPRPLY 324
QY 167 -----SYEQVRAF--PALTS-----LDLSDNPGLGERGLMAALCP 199
Db 325 FYDLSTLYSLTERVKRITVENSKVFLVPCLLSQHLKSLEYLDLSEN-LMVEEYLKNSACE 383
QY 200 HKFPAIQNALRNTGMEPTGVCALAAAG-----VOPHSLDLSHNSLRATVNSAPR- 252
Db 384 DAMPSLQTLILRQNL-----ASLEKTGETTLTLKNLINIDISKNSFH-----SMBET 431
QY 253 CMWSSALNSLNISFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELPEVDNLTLDGNPF 312
Db 432 COMPEKMYLNLSSTRIHSVTGCIPKTKLEILDVSNNNLNFSL--NLFPQKELYISRNKL 489
QY 313 L-VPGTAL 319
Db 490 MTLPDASL 497

Search completed: October 4, 2004, 16:51:23
Job time : 124 secs

ID	Q865B9	PRELIMINARY;	PRT; 1079 AA.
AC	Q865B9;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DD	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Toll-like receptor 9 protein.		
GN	TLR9.		
DN			
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID=9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Hasimoto M.;		
RT	"Molecular Cloning of canine TLR9 gene.";		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Hashimoto M.;		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB104899; BAC65192.1; --		
DR	GO; GO:0005622; C:intracellular; IEA.		
DR	GO; GO:0015025; C:membrane; IEA.		
DR	GO; GO:0005840; C:ribosome; IEA.		
DR	GO; GO:0003735; F:structural constituent of ribosome; IEA.		
DR	GO; GO:0003700; F:transcription factor activity; IEA.		
DR	GO; GO:0004888; P:transmembrane receptor activity; IEA.		
DR	GO; GO:0006412; P:protein biosynthesis; IEA.		
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA		
DR	InterPro; IPR000005; HTHAcC.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR003885; LRR_cyst.		
DR	InterPro; IPR003591; LRR_typ.		
DR	InterPro; IPR001266; Ribosomal_S19E.		
DR	InterPro; IPR00157; TIR.		
DR	Pfam; PF00560; LRR; 12		
DR	PRINTS; PR00019; LEURICHRPT.		
DR	Prodom; PD0003854; Ribosomal_S19E; 1.		
DR	SMART; SM00364; LRR_BAC; 4.		
DR	SMART; SM00366; LRR_PS; 10.		
DR	SMART; SM00365; LRR_SD22; 4.		
DR	SMART; SM00369; LRR_TYP; 16.		
DR	SMART; SM00255; TIR_1		
DR	PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.		
DR	PROSITE; PS0104; TIR; 1.		
KW	Receptor.		
SQ	SEQUENCE 1079 AA; 120349 MW; CA85D91D12D33CB8 CRC64;		

Query Match	8.1%	Score 148.5;	DB 6;	Length 1079;
Best Local Similarity	28.3%	Pred. No. 0.0032;		
Matches	90;	Conservative 48;	Mismatches 113;	Indels 67; Gaps 18;
Qy	71	RVRLITGAAQVPAQLLVGALRVLAYSELKLETLIEDLKITGTMPEPLPEATGLALSSURL	130	
Db	335	RLRLRN-----LSFNHYKKVSPFAHLHSLASSFGL-LSLQELDIHGIF	376	
Qy	131	RNVSWATGSMWLAELQQWLKGLKVLSTIAQAHSAPFSYEQVRAFPALTSLDLSDN--PGL	188	
Db	377	RLSETTLQS-LAHLPMQLRLHQLNFTISQAQLSIFG-----APGLRYVDSLSDNRISGA	430	
Qy	189	GE-----RGLMAALCPHK-FPAIQNLALRNTGMPETGVCAALAAAGVQPHSLDLSHNSLR	243	
Db	431	AEPAAATGEVADCGERWMPQSRDLALGPLG--TP-GSEAFMPSCRTLNFLLDLSRNL--	486	
Qy	244	ATVNP-----SAPFCWSSALNSLINSIFAGLEQVPKGLPAKLRVLDLSCHNRL--RAPQ	295	
Db	487	VTVQPFMFVRLARLQCGLGSH-NSISQAVNGSQFVPL---SNLRVLDLSHKNKLDLYHGRS	542	
Qy	296	PDELPEVDNLTLDCGN--PFLVPGT-----ALPHEGSMNSGVVPACARST	337	
Db	543	FTELPRIEALDLSYNSQFSPMRGVCHNLFSVAQLPALRYLSLAHNG-IHSRVSQOLRSAS	601	
Qy	338	L-SVGSVGTLLVLLQARG	354	

Db	602	LRALDFSGNTFSLMWAEG	619
RESULT 14			
Q9FHS6			
ID	Q9FHS6	PRELIMINARY;	PRT; 418 AA.
AC	Q9FHS6;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Similarity to elicitor-inducible receptor-like protein (Hypothetical protein).		
DE	NCBI_TaxID=3702;		
GN	Ar5G66330.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
FN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Columbia;		
FX	MEDLINE=20181125; PubMed=10718197;		
RA	Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,		
RA	Tabata S.,		
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence		
RT	features of the regions of 3,076,755 bp covered by sixty P1 and TAC		
RT	clones.";		
RT	DNA Res. 7:31-63(2000).		
FN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D.,		
RA	Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,		
RA	Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,		
RA	Hayaehizaki Y., Iehida J., Jones T., Kamiya A., Karlin-Neumann G.,		
RA	Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Seki M.,		
RA	Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,		
RA	Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,		
RA	Theologis A.;		
RT	"Full length cDNA of gene At5g66330 (GI:15239346)." ;		
RT	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
FN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,		
RA	Teng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,		
RA	Dang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,		
RA	Carninci P., Chen H., Cheuk R., Hayaehizaki Y., Iehida J., Jones T.,		
RA	Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,		
RA	Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,		
RA	Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,		
RA	Theologis A.;		
RT	"Arabidopsis Open Reading Frame (ORF) Clones." ;		
RT	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB022211; BAB10712.1; -		
DR	EWBL; AY065384; AAL38825.1; -		
DR	EMBL; AY117205; AAM51280.1; -		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR007090; LRR_plant.		
DR	Pfam; PF00560; LRR; 9.		
DR	PRINTS; PR00019; LEURICHRPT.		
DR	Hypothetical protein; Receptor.		
SW	SEQUENCE 418 AA; 45331 MW; 78C8876AF498C243 CRC64;		

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Query Match      8.0%; Score 148; DB 10; Length 418;
Best Local Similarity 24.2; Pred. No. 0.00098;
Matches 104; Conservative 55; Mismatches 106; Indels 164; Gaps 26;

Qy 4 EPCLEDD-----FRC-----VCNTEPQDMSEAFQCQSAVEIHHAGLNLEP 49
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 DPCDNIEFTFTCGFCDVVTGSGRVTELSLDQAGYSGSLSSV-----FNL-P 104

Ov 50 FLKRVIDAD--PROYADTVKAL--RVRRITVG-----AAOVPAOILLVGALRVIAYSRIKEL 102

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Db 1 IRGGSHSLDQPKGV--NTDPKQYADTIKALRVRRLKGAQAQVPAQLLVAVLRALGYSL 58
Qy 100 KELTLEDLKLTGTWPPPLPLEATGALSLRLRNYSWATGRSWLAELQWLKGLKVLISIA 159
Db 59 KELTLEDLVGTPTPTPTPLEATGPALTTLURNYSWATGGAWLGELQWLKGLKGRALNIA 118
Qy 160 QAHSFATSYEGVORAFPAALTSIDLNDPGLGERGLMAALCP 199
Db 119 QAHSFATPCAGLSTFEALTTLIDLNDPGLSGSLMAALCP 158

RESULT 10
Q8HY29 PRELIMINARY; PRT; 106 AA.
AC Q8HY29
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lipopolysaccharide receptor (Fragment).
GN CD14.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU=Blood;
RA Prgomet C., Sarikaya H., Bruckmaier R.M., Pfaffl M.W.;
RT "Isolation and characterisation of leukocyte subpopulations in ovine
RT blood and milk."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535322; CAD59477.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 1.
KW Receptor.
FT NON TER 1
FT NON TER 106
FT NON TER 106
SQ SEQUENCE 106 AA; 10973 MW; 4EEB025D18A96D8 CRC64;

Query Match 23.5%; Score 431.5; DB 6; Length 106;
Best Local Similarity 80.4%; Pred. No. 1.1e-27;
Matches 86; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Qy 179 SLDSNPNGLGERGLMAALCPKPAQNLALRNTGMEPTGVCALAAAGVQPHSLDLS 238
Db 1 TLDSNPNGLSGSLMAALCPKFPALQYLALRNTGMEPTGVCALAAAGVQPHSLDLS 60
Qy 239 HNSLRATVNPSPAPRCMSSALNSLNSLSPAGLEQVQPKGLPAKLRLVLDL 285
Db 61 HNSLRVTA-PGATRCVWPSALNSLNSLSPAGLEQVQPKGLTKLSVLDL 106

RESULT 11
Q88955 PRELIMINARY; PRT; 128 AA.
ID Q88955
AC Q88955;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Monocyte differentiation antigen CD14 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley; TISSU=Testis;
RX MEDLINE=20314485; PubMed=10854787;
RA Liu S., Shapiro R.A., Nie S., Zhu D., Vodovotz Y., Billiar T.R.;
RT "Characterization of rat CD14 promoter and its regulation by
RT transcription factors Ap1 and Sp family proteins in hepatocytes."

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RL Gene 250:137-147(2000).
DR EMBL; AF087944; AAC35372.1; -.
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14265 MW; 012C8DB034580234 CRC64;

Query Match 17.7%; Score 326; DB 11; Length 128;
Best Local Similarity 57.9%; Pred. No. 5.8e-19;
Matches 62; Conservative 18; Mismatches 25; Indels 2; Gaps 1;

Qy 2 TPEPCEL--DDEDPRVCNFPSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAAD 59
Db 21 TPEPCELDDQDESVRCYCNFSDPQPNWSSAFLCAGAEDEVFGGSRSELYLLKRVDTAN 80
Qy 60 PROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLRKELTLED 106
Db 81 LGQYTDIIRSLPLRLKLTVRSAVPTQLIFGLRLVGYSGLRRLTLEN 127

RESULT 12
Q940E8 PRELIMINARY; PRT; 613 AA.
ID Q940E8
AC Q940E8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fasciated ear2.
GN FEa2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21521230; PubMed=11641280;
RA Taguchi-Shiobara F., Yuan Z., Hake S., Jackson D.;
RT "The fasciated ear2 gene encodes a leucine-rich repeat receptor-like
RT protein that regulates shoot meristem proliferation in maize."
RL Genes Dev. 15:2755-2766(2001).
DR EMBL; AY055124; AALI7871.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 13.
DR PRINTS; PR00019; LEURICHRPT.
SQ SEQUENCE 613 AA; 63951 MW; 554A8A76C878A977 CRC64;

Query Match 8.2%; Score 151; DB 10; Length 613;
Best Local Similarity 27.9%; Pred. No. 0.00094;
Matches 81; Conservative 26; Mismatches 75; Indels 108; Gaps 15;

Qy 79 AAQVPAQLLVGALRVLAYSLRKELTLEDLKLTGTMPPLPLEATGLALSSLR--LRNVSWA 136
Db 4 ATPLPHQLLATFLVLVA-----SATQPAVPASTDRAALLAFRASLSPPSRA 49
Qy 137 TGRSWLAELQ-QWLKPGKLVLSIAQAHSPAPSYEQVRAFPALTSLDLSNPGLGERGLMA 195
Db 50 ALSWSGFLSPSWLG-----VSLHPATAPA-----PSVTT----- 79
Qy 196 ALCPHKFPAIQNLALRNTGMEPTGV-----CAALAAAGVQPHS----- 234
Db 80 -----PSVAELSLRGINL---TGVTPAAPALLRLRLTLDLSANALSGELPCSLPRSL 129
Qy 235 --LDLSHNSLRATVNPSPAPRCMSS--ALNSLNS--PAGLEQVQPK-GLPAKLRLVLDLSC 287
Db 130 LALDLSRNALSGAV-----FTCLPSSLPALRTLNLSANFLRLPLSPRLSPARLALDLSR 185
Qy 288 NLRNAPQPDDELPEVDN-----LTIDGNPFLLVPGTALPHEGSMNSGVVPA 332
Db 186 NAISGAVPEPRIVADPDNSALLLDDLSHNR-----SGEIPA 221

RESULT 13
Q865B9

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Db      248 RDAA--GAPSCDWPQNSLNLSFTGLKQVPGKGLPAKLSLLDLSYNRLDRNPSPDELPOV 305
QY      303 DNLTLGDNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLQAGRGF 355
Db      306 GNLSLKGPNFL---DSHSEKYNKSGVVTAGAPSSQAVALSGLTALLGLGDLRF 355

RESULT 7
Q920X9 PRELIMINARY; PRT; 356 AA.
ID Q920X9
AC Q920X9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=BFM/2Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039055; BAB68579.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICRPT.
FT NON TER 1
FT SEQUENCE 356 AA; 38049 MW; 8340094AB0962C1A CRC64;
SQ

Query Match 61.5%; Score 1131.5; DB 11; Length 356;
Best Local Similarity 65.4%; Pred. No. 4e-84;
Matches 231; Conservative 41; Mismatches 74; Indels 7; Gaps 3;

QY      3 PEPCLEDEDFRCVNFSEPPQDWSAEFCQCVSAVEVEITHAGLNLEPFLKRVADADPRQ 62
Db      10 PEPCLEDEES--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTTEADLQ 67
QY      63 YADTVKALRVRLTVGAQVPAQLLVGALRVLYASRLKELTLEDIKITGTWPPPLEATG 122
Db      68 FTDIISLSKRLTVRAARIESRILFGALRVLYGSLGQELTLENLEVTGTAPPPLEATG 127
QY      123 LALSRLRNVSATGRSWLAELQWLKPGKLVLSIAQAHPAFSVEQVRAFPALTSLDL 182
Db      128 PDNLNLRNVSWATRDWLAELQWLKPGKLVLSIAQAHPAFSVEQVRAFPALTSLDL 187
QY      183 SDNPLGERGLMAALCPHKFPAIQNALRNLTGMEPTGVCALAAAGVQPHSLDLSHNSL 242
Db      188 SDNPLGERGLISALCPKFPPTLQVLRNAGMETPSCVCSALAAARVQLQGLD----L 242
QY      243 RATVNPSPACRWMSSALNSLNSPAGLEQVPGKGLPAKLRVLDLSCNLRNRAPOQDELPEV 302
Db      243 RLRDAAGAPSCDWPQNSLNLSFTGLKQVPGKGLPAKLSVLDLSYNRLDRNPSPDELPOV 305
QY      303 DNLTLGDNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLQAGRGF 355
Db      306 GNLSLKGPNFL---DSHSEKYNKSGVVTAGAPSSQAVALSGLTALLGLGDLRF 355

RESULT 8
Q920X7 PRELIMINARY; PRT; 353 AA.
ID Q920X7
AC Q920X7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).

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OC      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=MSM/Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039058; BAB68582.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR NON TER 1
DR SEQUENCE 353 AA; 37812 MW; 3CF0FB707F29677B CRC64;
SQ

Query Match 59.9%; Score 1102; DB 11; Length 353;
Best Local Similarity 64.3%; Pred. No. 1e-81; 76; Indels 10; Gaps 3;
Matches 227; Conservative 40; Mismatches 40;

QY      3 PEPCLEDEDFRCVNFSEPPQDWSAEFCQCVSAVEVEITHAGLNLEPFLKRVADADPRQ 62
Db      10 PEPCLEDEES--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTTEADLQ 67
QY      63 YADTVKALRVRLTVGAQVPAQLLVGALRVLYASRLKELTLEDIKITGTWPPPLEATG 122
Db      68 FTDIISLSKRLTVRAARIESRILFGALRVLYGSLGQELTLENLEVTGTAPPPLEATG 127
QY      123 LALSRLRNVSATGRSWLAELQWLKPGKLVLSIAQAHPAFSVEQVRAFPALTSLDL 182
Db      128 PDNLNLRNVSWATRDWLAELQWLKPGKLVLSIAQAHPAFSVEQVRAFPALTSLDL 187
QY      183 SDNPLGERGLMAALCPHKFPAIQNALRNLTGMEPTGVCALAAAGVQPHSLDLSHNSL 242
Db      188 SDNPLGERGLISALCPKFPPTLQVLRNAGMETPSCVCSALAAARVQLQGLD----L 242
QY      243 RATVNPSPACRWMSSALNSLNSPAGLEQVPGKGLPAKLRVLDLSCNLRNRAPOQDELPEV 302
Db      243 RLRDAAGAPSCDWPQNSLNLSFTGLKQVPGKGLPAKLSVLDLSYNRLDRNPSPDELPOV 305
QY      303 DNLTLGDNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLQAGRGF 355
Db      303 GNLSLKGPNFL---DSHSEKYNKSGVVTAGAPSSQAVALSGLTALLGLGDLRF 355

RESULT 9
Q9YSE4 PRELIMINARY; PRT; 158 AA.
ID Q9YSE4
AC Q9YSE4;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE CD14 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RC SEQUENCE FROM N.A.
RA Steele B., Daniel J.A., Sartin J.L.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY289201; AAP43687.1; -.
FT NON TER 1
FT NON TER 158
FT SEQUENCE 158 AA; 16709 MW; 110AC213D4A97B4C CRC64;
SQ

Query Match 30.5%; Score 562; DB 6; Length 158;
Best Local Similarity 70.6%; Pred. No. 4.2e-38;
Matches 113; Conservative 16; Mismatches 29; Indels 2; Gaps 1;

QY      40 IHAGLNLEPFLKRVADADPRQYADTVKALRVRLTVGAQVPAQLLVGALRVLYASRL 99

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RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039060; BAB68584.1; -
DR EMBL; AB039062; BAB68586.1; -
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER 1
SQ SEQUENCE 356 AA; 38081 MW; 8FF604FDB09631AD CRC64;

Query Match 61.7%; Score 1135.5; DB 11; Length 356;
Best Local Similarity 65.7%; Pred. No. 1.9e-84;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;

Qy 3 PEPCELDDEDFRCVCFNFPSEPODMSAFQCVSAVEVEIHAGGLNLEPFLKRVDAADAPRQ 62
Db 10 PEPCELDEES--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTADLGQ 67
Qy 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTWPPPLEATG 122
Db 68 FTDIIKSLKRLTVRAARIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
Qy 123 LALSRLRLRVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTSIDL 182
Db 128 PDLNILNLRNVSWATRDWLAELQWLKPGKLVLSIAQAHSLNFSCEQVRVFPALSTIDL 187
Qy 183 SDNPGELGERGLMAALCPHKFPFAIQNALRLNTGMTPTGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPELGERGLISALCPKFPFTLVLRNAGMETPTSGVCSALAAARVOLQGLDLSHNSL 247
Qy 243 RATVNPSPAPRCWMSALNSLNSLSPAGLEQVPGKLPKLRVLDLSCNRLNRAPQDELPEV 302
Db 248 RDA--GAPSCDWPFSQNLNLSFTGLKQVPGKLPKLRVLDLSCNRLNRAPQDELPEV 305
Qy 303 DNLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOQARGF 355
Db 306 GNLSIKGNPFL--DSRSHSEKYNSSGVVTAGAPSSQVALSGTLALLLGDRLF 355

RESULT 5
Q91VC2 PRELIMINARY; PRT; 356 AA.
ID Q91VC2
AC Q91VC2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAST/El, and HMI/Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039063; BAB68587.1; -
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER 1
SQ SEQUENCE 356 AA; 38095 MW; 11041813429631B8 CRC64;

Query Match 61.5%; Score 1132.5; DB 11; Length 356;
Best Local Similarity 65.4%; Pred. No. 3.3e-84;
Matches 231; Conservative 41; Mismatches 74; Indels 7; Gaps 3;

Qy 3 PEPCELDDEDFRCVCFNFPSEPODMSAFQCVSAVEVEIHAGGLNLEPFLKRVDAADAPRQ 62
Db 10 PEPCELDEES--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTADLGQ 67
Qy 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTWPPPLEATG 122
Db 68 FTDIIKSLKRLTVRAARIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
Qy 123 LALSRLRLRVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTSIDL 182
Db 128 PDLNILNLRNVSWATRDWLAELQWLKPGKLVLSIAQAHSLNFSCEQVRVFPALSTIDL 187
Qy 183 SDNPGELGERGLMAALCPHKFPFAIQNALRLNTGMTPTGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPELGERGLISALCPKFPFTLVLRNAGMETPTSGVCSALAAARVOLQGLDLSHNSL 247
Qy 243 RATVNPSPAPRCWMSALNSLNSLSPAGLEQVPGKLPKLRVLDLSCNRLNRAPQDELPEV 302
Db 248 RDA--GAPSCDWPFSQNLNLSFTGLKQVPGKLPKLRVLDLSCNRLNRAPQDELPEV 305
Qy 303 DNLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOQARGF 355
Db 306 GNLSIKGNPFL--DSRSHSEKYNSSGVVTAGAPSSQVALSGTLALLLGDRLF 355

RESULT 6
Q920X6 PRELIMINARY; PRT; 356 AA.
ID Q920X6
AC Q920X6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus spicilegus (Steppe mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZBN;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039063; BAB68587.1; -
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON_TER 1
SQ SEQUENCE 356 AA; 38095 MW; 11041813429631B8 CRC64;

Query Match 61.5%; Score 1132.5; DB 11; Length 356;
Best Local Similarity 65.4%; Pred. No. 3.3e-84;
Matches 231; Conservative 41; Mismatches 74; Indels 7; Gaps 3;

Qy 3 PEPCELDDEDFRCVCFNFPSEPODMSAFQCVSAVEVEIHAGGLNLEPFLKRVDAADAPRQ 62
Db 10 PEPCELDEES--CSCNFSDPKPDWSSAFNCLGAADVLYGGRSLEYLLKRVDTADLGQ 67
Qy 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTWPPPLEATG 122
Db 68 FTDIIKSLKRLTVRAARIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
Qy 123 LALSRLRLRVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTSIDL 182
Db 128 PDLNILNLRNVSWATRDWLAELQWLKPGKLVLSIAQAHSLNFSCEQVRVFPALSTIDL 187
Qy 183 SDNPGELGERGLMAALCPHKFPFAIQNALRLNTGMTPTGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPELGERGLISALCPKFPFTLVLRNAGMETPTSGVCSALAAARVOLQGLDLSHNSL 247
Qy 243 RATVNPSPAPRCWMSALNSLNSLSPAGLEQVPGKLPKLRVLDLSCNRLNRAPQDELPEV 302
Db 248 RDA--GAPSCDWPFSQNLNLSFTGLKQVPGKLPKLRVLDLSCNRLNRAPQDELPEV 305
Qy 303 DNLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOQARGF 355
Db 306 GNLSIKGNPFL--DSRSHSEKYNSSGVVTAGAPSSQVALSGTLALLLGDRLF 355

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Db 138 GPPLSSLRNRVSWATGAWLAEQWLKPGKILSLIAQAHSLAFSCAQLHSFSAHLTLD 197
QY 182 LSDNPGELGRLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHNS 241
Db 198 LSDNPGELGRLIAALCPHKFPALRDALRNAGMTPTNGVCAMAAAGVQPHSLDLSHNS 257
QY 242 LRATVNPAPRCMWSALNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPE 301
Db 258 LSAAA-PGAPRCDFPSALSSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPE 316
QY 302 VDNLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 317 VSNLILDRNFDLPEAS--KQDQNSGVVAAACAHSAHSALTIGISTLALLRGAGDFA 369

```

RESULT 2

```

Q920X8
ID Q920X8 PRELIMINARY: PRT; 356 AA.
AC Q920X8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BLG2/Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039056; BAB68580.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON TER 1
SQ SEQUENCE 356 AA; 38169 MW; 8633BB9B2345D7A2 CRC64;

```

```

Query Match 62.0%; Score 1140.5; DB 11; Length 356;
Best Local Similarity 66.0%; Pred. No. 74e-85;
Matches 233; Conservative 40; Mismatches 73; Indels 7; Gaps 3;
QY 3 PEPCELDDEDFRCVCFNFPDPMSEAFQCVSAVEVEIHAGLNLEPFLKRVADADPRQ 62
Db 10 PEPCELDEE--RCSCNFSDPKPDMSAFNCLGAADVLYGGRSLEYLLKRVDTADLQ 67
QY 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLYSRLKELTLEDLKITGTWPPLEATG 122
Db 68 FTDIISLSLKLTVRAARIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
QY 123 LALSRLNRVSWATGRLWLAELQWLKPLKVLISIAQAHSPAFSYEQVRAFPALTSLDL 182
Db 128 PDNLILNRVSWATRDALWLAELQWLKPLKVLISIAQAHSLNFSCEQVRVPALSTLDL 187
QY 183 SDNPGELGRLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPGELGRLISALCPKLPFTLVQVLRNAGMETPTSGVCSALAAARVQLQGLDLSHNSL 247
QY 243 RATVNPAPRCMWSALNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPEV 302
Db 248 RDA--GAPSCDWPQLNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPEV 305
QY 303 DNLTLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGF 355
Db 306 GNLSLKGPNFL--DSESHSEKYNFSGVVTAGAPSSQVALLSGTLALLIGDLRF 355

```

RESULT 3

```

Q91VD3
ID Q91VD3 PRELIMINARY: PRT; 356 AA.
AC Q91VD3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWN/Msf, and NUL/Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;

```

```

Q91VD3
ID Q91VD3 PRELIMINARY: PRT; 356 AA.
AC Q91VD3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10SnJ, and pgn2;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RL Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039054; BAB68578.1; -.
DR EMBL; AB039059; BAB68583.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 2.
DR PRINTS; PR00019; LEURICHRPT.
FT NON TER 1
SQ SEQUENCE 356 AA; 38065 MW; 17CD94FDB09631B3 CRC64;

```

```

Query Match 61.8%; Score 1136.5; DB 11; Length 356;
Best Local Similarity 65.7%; Pred. No. 1.6e-84;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;
QY 3 PEPCELDDEDFRCVCFNFPDPMSEAFQCVSAVEVEIHAGLNLEPFLKRVADADPRQ 62
Db 10 PEPCELDEE--CSCNFSDPKPDMSAFNCLGAADVLYGGRSLEYLLKRVDTADLQ 67
QY 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLYSRLKELTLEDLKITGTWPPLEATG 122
Db 68 FTDIISLSLKLTVRAARIPSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEATG 127
QY 123 LALSRLNRVSWATGRLWLAELQWLKPLKVLISIAQAHSPAFSYEQVRAFPALTSLDL 182
Db 128 PDNLILNRVSWATRDALWLAELQWLKPLKVLISIAQAHSLNFSCEQVRVPALSTLDL 187
QY 183 SDNPGELGRLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHNSL 242
Db 188 SDNPGELGRLISALCPKLPFTLVQVLRNAGMETPTSGVCSALAAARVQLQGLDLSHNSL 247
QY 243 RATVNPAPRCMWSALNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPEV 302
Db 248 RDA--GAPSCDWPQLNSLNFAGLEQVPGKLPKALRVLDLSNRLNRAPOQDELPEV 305
QY 303 DNLTLTLDGNPFVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGF 355
Db 306 GNLSLKGPNFL--DSESHSEKYNFSGVVTAGAPSSQVALLSGTLALLIGDLRF 355

```

RESULT 4

```

Q91V69
ID Q91V69 PRELIMINARY: PRT; 356 AA.
AC Q91V69;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CD14 antigen (Fragment).
GN CD14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWN/Msf, and NUL/Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 117 Seconds
(without alignments)
960.038 Million cell updates/sec

Title: US-09-807-709D-1
Perfect score: 1840
Sequence: 1 TTEPCELDDEDFRCVNFPS.....TLSSGVSGTLVLQARGFA 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1338.5	72.7	369	6 Q9TTT3	Q9ttt3 equus caball
2	1140.5	62.0	356	11 Q920X8	Q920x8 mus musculu
3	1136.5	61.8	356	11 Q91VD3	Q91vd3 mus musculu
4	1135.5	61.7	356	11 Q91V69	Q91v69 mus musculu
5	1135.5	61.7	356	11 Q91VC2	Q91vc2 mus musculu
6	1132.5	61.5	356	11 Q920X6	Q920x6 mus spicile
7	1131.5	61.5	356	11 Q920X9	Q920x9 mus musculu
8	1102	59.9	353	11 Q920X7	Q920x7 mus musculu
9	562	30.5	158	6 Q7YS4	Q7yse4 ovis aries
10	431.5	23.5	106	6 Q8HY29	Q8hy29 ovis aries
11	326	17.7	128	11 Q88955	Q88955 rattus norv
12	151	8.2	613	10 Q940E8	Q940e8 zea mays (m
13	148.5	8.1	1079	6 Q865B9	Q865b9 canis faml
14	148	8.0	418	10 Q9FH56	Q9fh56 arabidopsis
15	147.5	8.0	586	4 Q8NI00	Q8ni00 homo sapien
16	144.5	7.9	353	4 Q9UJX9	Q9ujx9 homo sapien

17	144.5	7.9	353	4 Q8WUA8	Q8wua8 homo sapien
18	144	7.8	1535	5 Q9VPR0	Q9vpf0 drosophila
19	140.5	7.6	1178	10 Q942T3	Q942t3 oryza sativ
20	140.5	7.6	1274	10 Q8L1S5	Q8l1s5 oryza sativ
21	140	7.6	1121	10 Q942F3	Q942f3 oryza sativ
22	138	7.5	784	6 Q8MIQ3	Q8miq3 oryctolagus
23	137	7.4	1392	5 Q9VAD1	Q9vad1 drosophila
24	136.5	7.4	330	11 Q8K2A9	Q8k2a9 mus musculu
25	136.5	7.4	1007	10 Q9ZVD4	Q9zvd4 arabidopsis
26	135	7.3	1096	10 Q8S1D4	Q8s1d4 oryza sativ
27	134.5	7.3	1030	10 Q8H037	Q8h037 oryza sativ
28	133.5	7.3	833	10 Q852J5	Q852j5 oryza sativ
29	132	7.2	605	16 Q8ZH98	Q8zh98 yersinia pe
30	131.5	7.1	784	11 Q811T5	Q811t5 mus musculu
31	130.5	7.1	1110	10 Q94LN2	Q94ln2 oryza sativ
32	130	7.1	290	2 Q8KNJ6	Q8knj6 micromonosp
33	130	7.1	1024	16 Q8XS09	Q8xs09 ralstonia s
34	129	7.0	1143	10 Q9SUB9	Q9sub9 arabidopsis
35	128.5	7.0	342	11 Q91XL1	Q91xl1 mus musculu
36	128.5	7.0	497	10 Q7XKC0	Q7xkc0 oryza sativ
37	128.5	7.0	784	11 Q8K3D9	Q8k3d9 mus musculu
38	128.5	7.0	1013	10 Q8LQ10	Q8lq10 oryza sativ
39	128	7.0	291	16 Q8ZH99	Q8zh99 yersinia pe
40	128	7.0	444	4 Q9H5H8	Q9h5h8 homo sapien
41	128	7.0	453	4 Q86XY1	Q86xy1 homo sapien
42	128	7.0	601	13 Q7SXW3	Q7sxw3 brachydanio
43	128	7.0	622	4 Q8N3E0	Q8n3b0 homo sapien
44	128	7.0	797	4 Q9UGS3	Q9ugs3 homo sapien
45	127.5	6.9	905	10 Q64757	Q64757 arabidopsis

ALIGNMENTS

RESULT 1

Q9TTT3 ID Q9TTT3 PRELIMINARY; PRT; 369 AA.
AC Q9TTT3;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Lipopolysaccharide receptor.
GN CD14.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactylia; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vanderplas M.L., Barton M.H., Tobias P.S., Moore J.N.;
RT "Cloning of the equine CD14 receptor and determination of its full-length cDNA sequence."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200416; AAF08963.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 1.
KW Receptor.
SQ SEQUENCE 369 AA; 39108 MW; F72B4168114A9ED3 CRC64;

Query Match 72.7%; Score 1338.5; DB 6; Length 369;
Best Local Similarity 74.6%; Pred. No. 5.3e-101;
Matches 265; Conservative 30; Mismatches 55; Indels 5; Gaps 3;

Qy	2	TPEPCELDDEDFRCVNFSPQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADPR	61
Db	20	TLEPCEVDENFRVCNFTGPDWSSAFQCMTAVEIRGGRNLEQFLK--GASADPK	77
Qy	62	QYADTVKALRVRLTVGAQVPAQLVGCALRVLAYSLKELTLEDLKLTGTMPPLPLBAT	121
Db	78	QYADIVKALRQLRITVGAQVPAQLVGCALRVLAYSLKELTLEDLKLTGTMPPLPLBAT	137
Qy	122	GLALSRLRNVSQWATGRSWLAELQQLKPLKVLISIAQAHSAPFSYEQVRAFPALTSLD	181

Db 97 RQYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 156
 Qy 121 TGLALSSLRRLNVSWATGRSWLAELQQLKPKLVLSIAQAHSAPFSYEQVRAPALTS 180
 Db 157 TGLALSSLRRLNVSWATGRSWLAELQQLKPKLVLSIAQAHSAPFSYEQVRAPALTS 216
 Qy 181 DLSNPGGLGERGLMAALCPHKFPATONLALRNTGMETGTGCAALAAAGVQPHSLDLSHN 240
 Db 217 DLSNPGGLGERGLMAALCPHKFPATONLALRNTGMETGTGCAALAAAGVQPHSLDLSHN 276
 Qy 241 SLRATVNPSPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDLP 300
 Db 277 SLRATVNPSPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDLP 336
 Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTFLVLQGAR 353
 Db 337 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTFLVLQGAR 389

RESULT 15

AAR98576
 ID AAR98576 standard; peptide; 348 AA.

XX AAR98576;

XX 07-FEB-1997 (first entry)

XX CD14 sequence.

XX Antinflammatory; lipopolysaccharide; LPS; Gram-positive bacteria; CD14;
 KW treatment; septic shock; inflammatory bowel disease; liver failure;
 KW graft versus host disease; pancreatitis; tuberculosis;
 XX adult respiratory distress syndrome; detection; quantification.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain

FT 1..56 /label= EGF-like domain

FT Disulfide-bond

FT 6..15 Disulfide-bond

FT 15..17 Disulfide-bond

FT 17..32 Disulfide-bond

FT Modified-site 18 /note= "Potential N-linked glycosylation site"

FT Region 57..64 /label= Linker

FT Region 65..283 /label= Core region

FT Disulfide-bond 168..198

FT Disulfide-bond 222..253

FT Modified-site 263 /note= "Potential N-linked glycosylation site"

FT Region 284..348 /label= Tail

FT Disulfide-bond 287..333

FT Modified-site 304 /note= "Potential N-linked glycosylation site"

XX WO9620956-A1.

XX 11-JUL-1996.

XX 28-DEC-1995; 95WO-US016977.

XX 30-DEC-1994; 94US-00366953.

XX (AMGE-) AMGEN INC.

XX (UYRQ) UNIV ROCKEFELLER.

XX Lichenstein HS, Wright SD, Narhi LO, Juan S;

XX WPI; 1996-333943/33.

XX
 PT Peptide(s) based on CD14 sequences - which bind to lipo:poly:saccharide
 PT and inhibit CD14 mediated inflammatory responses.
 XX Disclosure; Fig 1; 103pp; English.
 XX Antinflammatory peptides based on the human CD14 sequence (See AAR98570-
 CC 75 and AAR98577-80) can bind to lipopolysaccharide (LPS) and inhibit
 CC binding of LPS or Gram positive cell components to CD14, thus reducing or
 CC eliminating CD14 mediated inflammatory responses. They can be used for
 CC treating inflammatory conditions in particular, septic shock,
 CC inflammatory bowel disease, acute and chronic liver failure, graft versus
 CC host disease, intestinal or liver transplant, adult respiratory distress
 CC syndrome, acute pancreatitis and tuberculosis. They can also be used to
 CC remove, detect or quantitate LPS or Gram-positive cell components in
 CC samples. The peptides are used in doses of 0.1-100 mg/kg by parenteral or
 CC oral routes
 XX SQ Sequence 348 AA;

Query Match 97.3%; Score 1791; DB 2; Length 348;
 Best Local Similarity 99.7%; Pred. No. 2.5e-164;
 Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	TTPEPCELDDDEPRVCNFESEPOPDWSEAFQCVSAVEIHAGGLNLEPFLKRYDADADP	60
Db	1	TTPEPCELDDDEPRVCNFESEPOPDWSEAFQCVSAVEIHAGGLNLEPFLKRYDADADP	60
Qy	61	RQYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA	120
Db	61	RQYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA	120
Qy	121	TGLALSSLRRLNVSWATGRSWLAELQQLKPKLVLSIAQAHSAPFSYEQVRAPALTS	180
Db	121	TGLALSSLRRLNVSWATGRSWLAELQQLKPKLVLSIAQAHSAPFSYEQVRAPALTS	180
Qy	181	DLSNPGGLGERGLMAALCPHKFPATONLALRNTGMETGTGCAALAAAGVQPHSLDLSHN	240
Db	181	DLSNPGGLGERGLMAALCPHKFPATONLALRNTGMETGTGCAALAAAGVQPHSLDLSHN	240
Qy	241	SLRATVNPSPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDLP	300
Db	241	SLRATVNPSPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDLP	300
Qy	301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTFLVL	348
Db	301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTFLVL	348

Search completed: October 4, 2004, 16:53:33
 Job time : 130 secs

ID AAW41693 standard; protein; 375 AA.
XX AAW41693;
AC
XX
XX 01-MAY-1998 (first entry)
XX
XX Human CD14.
XX
XX Identification; binding inhibitor; lipopolysaccharide; LPS; CD14;
KW binding protein; LBP; monocyte receptor; treatment; septic shock; human.
XX
XX Homo sapiens.
OS
XX US5705398-A.
PN
XX
XX 06-JAN-1998.
PD
XX
XX 02-MAR-1994; 94US-00205719.
PF
XX
XX 02-MAR-1994; 94US-00205719.
PR
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX
XX Tobias P, Mintz DN, Ulevitch R;
PI
XX
XX WPI; 1998-086145/08.
DR
XX
XX N-PSDB; AAV05505.
DR
XX
XX Assay for lipo:poly:saccharide binding inhibitors - useful in the
PT treatment of septic shock and other lipo:poly:saccharide-mediated
PT disorder(s).
PT
XX
XX
XX Claim 9; Col 19-22; 21pp; English.
PS
XX
XX The present sequence was used in the development of a novel method for
CC identifying a compound that inhibits the binding of a lipopolysaccharide
CC (LPS) to a LPS-binding protein (LBP), or LBP-dependent binding of LPS to
CC monocyte receptor CD14. The method comprises measuring the fluorescence
CC emitted by a reaction mixture containing fluoresceinated LPS, isolated
CC LBP and optionally CD14 in the presence and absence of the compound, and
CC identifying the compound as an inhibitor if the fluorescence emitted by
CC the reaction mixture containing the compound is less than that emitted by
CC the reaction mixture that does not contain the compound. The method can
CC be used to identify drugs useful for treating septic shock and related
CC LPS-mediated disorders
XX
SQ Sequence 375 AA;
Query Match 99.2%; Score 1826; DB 2; Length 375;
Best Local Similarity 99.4%; Pred. No. 1.1e-167; Indels 0; Gaps 0;
Matches 354; Conservative 0; Mismatches 2;
QY 1 TTPEPCBLDDEDFRCVCFSEPDWSEAFQCVSAVEIHHAGLNLEPFLKRYDADADP 60
DB 20 TTPEPCBLDDEDFRCVCFSEPDWSEAFQCVSAVEIHHAGLNLEPFLKRYDADADP 79
QY 61 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKITGTMPPLPLEA 120
DB 80 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKITGTMPPLPLEA 139
QY 121 TGLALSSLRNVSWSATGRSWLAEQWLKPLGLKVLISIAQAHSPAFSYEQVRAFPALTS 180
DB 140 TGLALSSLRNVSWSATGRSWLAEQWLKPLGLKVLISIAQAHSPAFSYEQVRAFPALTS 199
QY 181 DLSNPGGLGRLMAALCPHKFPAIONLALNTGWTPTGVCAALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGGLGRLMAALCPHKFPAIONLALNTGWTPTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPELP 300
DB 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPELP 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356

DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 375
RESULT 14
AAB58147
ID AAB58147 standard; protein; 431 AA.
XX
XX AAB58147;
AC
XX
XX 14-MAR-2001 (first entry)
DT
XX
XX Lung cancer associated polypeptide sequence SEQ ID 485.
DE
XX
XX Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.
XX
XX Homo sapiens.
OS
XX WO200055180-A2.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 08-MAR-2000; 2000WO-US005918.
PF
XX
XX 12-MAR-1999; 99US-0124270P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX (ROSE/) ROSEN C A.
XX
XX Ruben SM;
PI
XX
XX WPI; 2000-587514/55.
DR
XX
XX N-PSDB; AAF18023.
DR
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer.
PT
XX
XX
XX Claim 11; Page 967-968; 1425pp; English.
XX
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the protein
CC or polynucleotide sequences. The lung cancer associated polynucleotide
CC sequences may be used for detection of lung cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The proteins may be used to treat disorders such as
CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
CC cardiovascular, renal, and proliferative disorders. The proteins may also
CC be used in the treatment of wounds and infectious diseases.
CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
CC used in the course of the invention for the identification and
CC characterisation of the polynucleotide and protein sequences
XX
SQ Sequence 431 AA;
Query Match 98.2%; Score 1807; DB 3; Length 431;
Best Local Similarity 99.2%; Pred. No. 9.6e-166;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTPEPCBLDDEDFRCVCFSEPDWSEAFQCVSAVEIHHAGLNLEPFLKRYDADADP 60
DB 37 TTPEPCBLDDEDFRCVCFSEPDWSEAFQCVSAVEIHHAGLNLEPFLKRYDADADP 96
QY 61 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKITGTMPPLPLEA 120

PN WO2003057160-A2.
 XX 17-JUL-2003.
 PD 30-DEC-2002; 2002WO-US041798.
 PF 02-JAN-2002; 2002US-0345444P.
 XX 25-JAN-2002; 2002US-0351885P.
 PR 25-FEB-2002; 2002US-0360066P.
 PR 05-MAR-2002; 2002US-0362004P.
 PR 20-MAR-2002; 2002US-0366869P.
 PR 21-MAR-2002; 2002US-0366284P.
 PR 28-MAR-2002; 2002US-0368679P.
 PR 19-AUG-2002; 2002US-0404809P.
 PR 21-AUG-2002; 2002US-0405645P.
 XX (GETH) GENENTECH INC.
 PA Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;
 XX Williams PM, Wu TD, Zhang Z;
 PI WPI; 2003-569537/53.
 DR N-PSDB; ADD89093.
 DR
 XX New antibodies against tumor-associated antigenic target polypeptide,
 PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
 PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
 PT carcinomas.
 XX
 PS Claim 1; SEQ ID NO 23; 252pp; English.
 XX
 CC The present invention relates to antibodies against tumour-associated
 CC antigenic target polypeptide. The antibody is useful for treating or
 CC diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung
 CC cancer, breast cancer, colon cancer, ovarian cancer, prostate
 CC adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The
 CC present sequence represents a TAT polypeptide.
 XX
 SQ Sequence 375 AA;
 Query Match 99.5%; Score 1831; DB 7; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.8e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDFRCVCFNFSEFPQDWEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 60
 Db 20 TTPEPCELDDDFRCVCFNFSEFPQDWEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 79
 QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 120
 Db 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 139
 QY 121 TGLALSSRLRNYSWATGRSWLAELQWLKPGKLVLSIAQHSAPFSYEQVRAPPALTSL 180
 Db 140 TGLALSSRLRNYSWATGRSWLAELQWLKPGKLVLSIAQHSAPFSYEQVRAPPALTSL 199
 QY 181 DLSNDFGLGRLMAALCPHKFPFPAIONLALRNTGNETPTGVCALAAGVQPHSLDLSHN 240
 Db 200 DLSNDFGLGRLMAALCPHKFPFPAIONLALRNTGNETPTGVCALAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLDLSNRLNRAFPQDPELP 300
 Db 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLDLSNRLNRAFPQDPELP 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVLOGARGFA 356
 Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVLOGARGFA 375
 RESULT 12
 ID AAO22313
 XX AAO22313 standard; protein; 356 AA.

AC AAO22313;
 XX 11-OCT-2002 (first entry)
 DT Anti-CD14 monoclonal antibody related protein SEQ ID No 1.
 DE Immunosuppressive; antibacterial; anti-CD14 antibody; epitope; sepsis;
 KW human CD14.
 XX Homo sapiens.
 OS WO200242333-A1.
 PN 30-MAY-2002.
 PD 28-SEP-2001; 2001WO-JP008563.
 PF 22-NOV-2000; 2000JP-00356719.
 XX (MOCH) MOCHIDA PHARM CO LTD.
 PA Furusako S, Shirakawa K, Mori S;
 XX WPI; 2002-454920/48.
 DR Anti-CD14 monoclonal antibody which inhibits CD14/T lymphocyte receptor
 PT binding by specifically recognizing epitope in human CD14 domain to
 PT prevent interaction and suppress cell activation, useful for treating
 PT sepsis.
 XX
 PS Claim 10; Page 109-112; 156pp; Japanese.
 XX The invention relates to an anti-CD14 antibody which can specifically
 CC recognise an epitope containing a part of a domain with not less than 8
 CC amino acids in human CD14 in the region from positions 269-315 in a fully
 CC defined sequence of 356 amino acids as given in the specification. The
 CC antibody is useful in drug compositions for treating sepsis and for
 CC screening remedies for sepsis. This sequence represents an anti-CD14
 CC related protein of the invention
 XX
 SQ Sequence 356 AA;
 Query Match 99.3%; Score 1827; DB 5; Length 356;
 Best Local Similarity 99.4%; Pred. No. 8.5e-168;
 Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDFRCVCFNFSEFPQDWEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 60
 Db 1 TTPEPCELDDDFRCVCFNFSEFPQDWEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 60
 QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 120
 Db 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPPLEA 120
 QY 121 TGLALSSRLRNYSWATGRSWLAELQWLKPGKLVLSIAQHSAPFSYEQVRAPPALTSL 180
 Db 121 TGLALSSRLRNYSWATGRSWLAELQWLKPGKLVLSIAQHSAPFSYEQVRAPPALTSL 180
 QY 181 DLSNDFGLGRLMAALCPHKFPFPAIONLALRNTGNETPTGVCALAAGVQPHSLDLSHN 240
 Db 181 DLSNDFGLGRLMAALCPHKFPFPAIONLALRNTGNETPTGVCALAAGVQPHSLDLSHN 240
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLDLSNRLNRAFPQDPELP 300
 Db 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLVLDLSNRLNRAFPQDPELP 300
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVLOGARGFA 356
 Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVLOGARGFA 356
 RESULT 13
 AAW41693

CC number therefore none of the sequences can be explicitly identified.
XX
SQ Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 7; Length 375;
Best Local Similarity 99.7%; Pred. No. 3.8e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDPRVCNFSFSEPODSEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDPRVCNFSFSEPODSEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 79

QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKELTLEDKTI GTMPPLPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKELTLEDKTI GTMPPLPLEA 139

QY 121 TGLALSSRLRLNVSWATGRSWLAELQWLKPLKVLISIAQAHSPAFSVEQVRAFPALTSL 180
Db 140 TGLALSSRLRLNVSWATGRSWLAELQWLKPLKVLISIAQAHSPAFSVEQVRAFPALTSL 199

QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALNTGMTPTGVCALAAGVOPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPAIQNLALNTGMTPTGVCALAAGVOPHSLDLSHN 259

QY 241 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 319

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 375

RESULT 10
ADE55388
ID ADE55388 standard; protein; 375 AA.
XX
AC ADE55388;
DT 29-JAN-2004 (first entry)
DE Human Protein CAA29999, SEQ ID NO 1203.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN W02003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GRHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; CAA29999.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat

or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 7; Length 375;
Best Local Similarity 99.7%; Pred. No. 3.8e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDPRVCNFSFSEPODSEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDPRVCNFSFSEPODSEAFQCVSAVEVEIHAGLNLEPFLKRVDAADP 79

QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKELTLEDKTI GTMPPLPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKELTLEDKTI GTMPPLPLEA 139

QY 121 TGLALSSRLRLNVSWATGRSWLAELQWLKPLKVLISIAQAHSPAFSVEQVRAFPALTSL 180
Db 140 TGLALSSRLRLNVSWATGRSWLAELQWLKPLKVLISIAQAHSPAFSVEQVRAFPALTSL 199

QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALNTGMTPTGVCALAAGVOPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPAIQNLALNTGMTPTGVCALAAGVOPHSLDLSHN 259

QY 241 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 319

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLLQGARGFA 375

RESULT 11
ADD89019
ID ADD89019 standard; protein; 375 AA.
XX
AC ADD89019;
XX
DT 29-JAN-2004 (first entry)
XX
DE TAT258.
XX
KW tumour-associated antigenic target polypeptide; Cytostatic; tumour;
KW cancer.
XX
OS Homo sapiens.
XX

PN WO200235236-A1.
 XX 02-MAY-2002.
 XX 26-OCT-2001; 2001WO-FR003352.
 XX 27-OCT-2000; 2000FR-00013883.
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX Jeannin P, Magistrelli G, Herbault N, Bonnefoy J;
 XX WPI: 2002-383586/41.
 DR N-PSDB; AEN83319.
 XX
 PT Identifying agent that binds to scavenger receptors and signals through a
 PT Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
 PT cytotoxic T cell response.
 XX
 PS Disclosure; Page 62-63; 71pp; French.
 XX
 CC The present invention relates to a method for identifying new therapeutic
 CC compounds (I) by selecting molecules that bind to scavenger receptors and
 CC signal through a Toll receptor. The present sequence is the protein
 CC sequence for human CD14, which was used to illustrate the method of the
 CC invention. (I) are useful as carriers and/or adjuvants in prophylactic or
 CC therapeutic vaccines, particularly where the antigen is derived from a
 CC virus, bacterium, yeast, fungus, parasite or tumour cell, especially a
 CC pathogen that causes respiratory tract infection, also more generally a
 CC inducing an immune response. (I) can also be used for specific targeting
 CC of active agents (antigens etc.) to antigen-presenting cells (especially
 CC immature dendritic cells), for subsequent internalisation by these cells
 XX.
 SQ Sequence 375 AA;
 Query Match 99.5%; Score 1831; DB 5; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.8e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPPECELDDEDFRCVNFSEFQVSAVEVEIHAGGVLNLEPFLKRVVDADADP 60
 Db 20 TTPPECELDDEDFRCVNFSEFQVSAVEVEIHAGGVLNLEPFLKRVVDADADP 79
 QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKLTLEDLKITGTMPPLEA 120
 Db 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKLTLEDLKITGTMPPLEA 139
 QY 121 TGLALSSLRNNSWATGRSWLAELQWLKPGKLVLSIAQHSFAPSCQVRAPFALTSL 199
 Db 140 TGLALSSLRNNSWATGRSWLAELQWLKPGKLVLSIAQHSFAPSCQVRAPFALTSL 199
 QY 181 DLSNPGGLGERGLMAALCPHKFPAIONLALNTQMETPTGVCALAAGVQPHSLDLSHN 240
 Db 200 DLSNPGGLGERGLMAALCPHKFPAIONLALNTQMETPTGVCALAAGVQPHSLDLSHN 259
 QY 241 SLRATNPSPRCMWSALNSLNSFAGLEQVPGKLPALRVLDLSNRLNRAPOQDDEL 300
 Db 260 SLRATNPSPRCMWSALNSLNSFAGLEQVPGKLPALRVLDLSNRLNRAPOQDDEL 319
 QY 301 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTIVLLQGARGFA 356
 Db 320 EVNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTIVLLQGARGFA 375
 RESULT 9
 ADD25617
 ID ADD25617 standard; protein; 375 AA.
 XX
 AC ADD25617;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Binding domain-immunoglobulin fusion protein-associated protein #86.

XX
 KW Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX
 OS Unidentified.
 XX
 XX US2003118592-A1.
 XX
 PD 26-JUN-2003.
 XX
 PF 25-JUL-2002; 2002US-00207655.
 XX
 PR 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX
 XX (GENE-) GENE-CRAFT INC.
 XX
 PA Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 XX
 XX WPI: 2003-801317/75.
 XX
 PT New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 178; 157pp; English.
 XX
 CC The invention relates to a binding domain-immunoglobulin fusion protein
 CC comprising a binding domain polypeptide that is fused to an
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
 CC CH2 constant region polypeptide that is fused to the hinge region
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
 CC polypeptide that is fused to the CH2 constant region polypeptide. The
 CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an
 CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide (operably linked to a promoter),
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID

PT Recombinant DNA encoding myelomonocytic differentiation antigen CD14 -
 PT used for producing recombinant CD14 for use in e.g. diagnosis of myeloid
 PT disorders such as leukaemia.

XX Claim 1; Fig 3; 11pp; English.

XX Human myelomonocytic differentiation antigen CD14 (AA05316) is an
 CC antigen useful in the diagnosis of mature myeloid leukemia. Its amino
 CC acid sequence was deduced from a cDNA clone (AA139717) obtd. by screening
 CC COS 7 cell transfectants with monoclonal antibodies to CD14. Large ants.
 CC of CD14 can be produced by expression in transformed host cells; mature,
 CC glycosylated CD14 is produced in mammalian host cells, and
 CC nonglycosylated CD14 in prokaryotic hosts. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 2; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.8e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
 Db |||||
 20 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
 QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
 Db |||||
 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
 QY 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLGLVLSIAQAHSPAFSVEQVRAPFALTS 180
 Db |||||
 140 TGLALSSLRNRVSWATGRSWLAELQWLKPLGLVLSIAQAHSPAFSVEQVRAPFALTS 199
 QY 181 DLSNPGIGERGLMAALCPHKFPAIQNLALRNTGNETPTGVCALAAGVQPHSLDLSHN 240
 Db |||||
 200 DLSNPGIGERGLMAALCPHKFPAIQNLALRNTGNETPTGVCALAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPELP 300
 Db |||||
 260 SLRATVNSAPRCMWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPELP 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
 Db |||||
 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 375

RESULT 7

AAG68129
 ID AAG68129 standard; protein; 375 AA.

XX AAG68129;

AC AAG68129;

DT 23-JAN-2002 (first entry)

DE Human CD14 related protein sequence SEQ ID NO:3.
 XX Human; Toll like receptor; TLR; CD14; antibody; anti-CD14 antibody;
 KW TLR/CD14 binding inhibitor; antibacterial; immunosuppressive;
 KW antipyretic; hypertensive; immunostimulant; haemostatic; vasotropic;
 KW bacterial infection; sepsis; fever; hypotension; leukopenia;
 KW thrombopenia; shock; multi-organ failure.

XX Homo sapiens.

OS WO200172993-A1.

PN 04-OCT-2001.

PD 02-APR-2001; 2001WO-JP002869.

PF 31-MAR-2000; 2000JP-00099617.

PR 22-NOV-2000; 2000JP-00356719.

PR 28-MAR-2001; 2001US-00806159.

XX (MOCH) MOCHIDA PHARM CO LTD.

XX Furusako S, Mori S, Shirakawa K, Takahashi T;

XX WPI; 2001-616487/71.

XX N-PSDB; AAI71230.

XX Anti-CD14 antibody or its fragment inhibiting the binding of CD14 to Toll
 PT -like receptor, applicable in drugs for treating bacterial infection as
 PT well as sepsis, fever, hypotension, leukopenia, thrombopenia and shock.

XX Disclosure; Page 156-160; 202pp; Japanese.

XX The present invention describes an anti-CD14 antibody, which has a
 CC function of inhibiting the binding of CD14 to the Toll-like receptor
 CC (TLR). The anti-CD14 antibody can specifically recognise the epitope
 CC containing the domain from numbers 269-315 in human CD14 of the sequence
 CC in AAG68127 or a part of it. Anti-CD14 antibody has antibacterial,
 CC immunosuppressive, antipyretic, hypertensive, immunostimulant,
 CC haemostatic and vasotropic activities. The antibody together with other
 CC polypeptides are applicable in drugs for treating bacterial infection as
 CC well as sepsis, fever, hypotension, leukopenia, thrombopenia, shock and
 CC multi-organ failure. AAG68127 to AAG68137 and AAI71230 to AAI71295
 CC represent sequences used in the exemplification of the present invention

XX Sequence 375 AA;

Query Match 99.5%; Score 1831; DB 4; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.8e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
 Db |||||
 20 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
 QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
 Db |||||
 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
 QY 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLGLVLSIAQAHSPAFSVEQVRAPFALTS 180
 Db |||||
 140 TGLALSSLRNRVSWATGRSWLAELQWLKPLGLVLSIAQAHSPAFSVEQVRAPFALTS 199
 QY 181 DLSNPGIGERGLMAALCPHKFPAIQNLALRNTGNETPTGVCALAAGVQPHSLDLSHN 240
 Db |||||
 200 DLSNPGIGERGLMAALCPHKFPAIQNLALRNTGNETPTGVCALAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPELP 300
 Db |||||
 260 SLRATVNSAPRCMWSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPELP 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 356
 Db |||||
 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLLQGARGFA 375

RESULT 8

ABB83163

ID ABB83163 standard; protein; 375 AA.

XX ABB83163;

AC ABB83163;

DT 09-AUG-2002 (first entry)

DE Human CD14.

XX Human; virucide; antibacterial; fungicide; parasiticide; receptor;
 KW cytostatic; immunostimulatory; scavenger receptor; Toll receptor;
 KW respiratory tract infection; CD14.

XX Homo sapiens.

XX

Db 121 TGLALSSLRNRVSWATGRSWLAELQWLKPGKVLSTIAQHSAPFSCQVRAFPALTSL 180
QY 181 DLSNDPGLGERGLMAALCPHKFPFAIQNLALRNTGMTPTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNDPGLGERGLMAALCPHKFPFAIQNLALRNTGMTPTGVCAALAAAGVQPHSLDLSHN 240
QY 241 SURATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 241 SURATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTIVLLQGARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTIVLLQGARGFA 356
RESULT 5
AAB73984
ID AAB73984 standard; protein; 356 AA.
XX AAB73984;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human soluble CD14 protein.
KW Human; CD14; soluble; fractional quantification; septicemia; diagnosis.
XX Homo sapiens.
OS
PN WO200122085-A1.
XX
PN- 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-JP006359.
XX
PR 17-SEP-1999; 99JP-00264474.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
PI Furusako S, Shirakawa K;
XX
DR WPI; 2001-258042/26.
XX
PT Highly-sensitive, convenient and specific method for fractional
PT measurement of soluble CD14 protein in body fluid, with use of antibody,
PT applicable in diagnosis of septicemia.
XX
PS Claim 6; Page 56-57; 64pp; Japanese.
XX
CC The present sequence is a soluble human CD14 protein. It is provided in a
CC specification relating to a highly-sensitive, convenient and specific
CC method for fractional measurement of a soluble CD14 protein having a low
CC molecular weight in a body fluid. The method comprises measuring total
CC soluble CD14 proteins, measuring a specific soluble CD14 protein having a
CC high molecular weight, and subtracting the value of the measurement of
CC the total proteins by that of the specific protein. The method is useful
CC for the fractional quantitation of a soluble CD14 protein having a low
CC molecular weight in a body fluid. It is also useful for the qualitative
CC and quantitative determination of soluble CD14 protein having a high
CC molecular weight, which is applicable in diagnosis of septicemia
XX
SQ Sequence 356 AA;
Query March 99.5%; Score 1831; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 3.5e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTPPELDDDDDFRCVNFSEPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRYVDADADP 60
Db 1 TTPPELDDDDDFRCVNFSEPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRYVDADADP 60
QY 61 ROYADTVKALRVRLTVGAAGVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120

Db 61 ROYADTVKALRVRLTVGAAGVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
QY 121 TGLALSSLRNRVSWATGRSWLAELQWLKPGKVLSTIAQHSAPFSCQVRAFPALTSL 180
Db 121 TGLALSSLRNRVSWATGRSWLAELQWLKPGKVLSTIAQHSAPFSCQVRAFPALTSL 180
QY 181 DLSNDPGLGERGLMAALCPHKFPFAIQNLALRNTGMTPTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNDPGLGERGLMAALCPHKFPFAIQNLALRNTGMTPTGVCAALAAAGVQPHSLDLSHN 240
QY 241 SURATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 241 SURATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTIVLLQGARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTIVLLQGARGFA 356
RESULT 6
AAW05316
ID AAW05316 standard; protein; 375 AA.
XX AAW05316;
XX
DT 25-MAR-2003 (revised)
DT 03-JAN-1997 (first entry)
XX
DE Myelomonocytic differentiation antigen CD14.
XX
KW Myelomonocytic differentiation antigen; CD14; myeloid leukaemia;
KW diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Modified-site 37..39 /label= Sig_peptide
FT /label= Glycosylation
FT Modified-site 151..153 /note= "potential N-linked glycosylation site"
FT /label= Glycosylation
FT Modified-site 266..268 /note= "potential N-linked glycosylation site"
FT /label= Glycosylation
FT Modified-site 282..284 /note= "potential N-linked glycosylation site"
FT /label= Glycosylation
FT Modified-site 323..325 /note= "potential N-linked glycosylation site"
FT /label= Glycosylation
FT /note= "potential N-linked glycosylation site"
XX US5543303-A.
XX
PD 06-AUG-1996.
XX
PF 13-DEC-1993; 93US-00165583.
XX
PR 28-NOV-1988; 88US-00276794.
PR 08-JUN-1990; 90US-00536163.
PR 06-NOV-1991; 91US-00787763.
PR 22-JUL-1992; 92US-00916806.
XX
PA (GOYE/) GOYERT S M.
XX
PI Goyert SM;
XX
DR WPI; 1996-370638/37.
DR N-PSDB; AAT39716, AAT39717.
XX

KW antiarteriosclerotic; vulnery; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing.

OS Homo sapiens.
 XX
 XX WO2003018621-A2.
 PN
 XX
 XX 06-MAR-2003.
 PD
 XX
 XX 23-AUG-2002; 2002WO-GB003892.
 PF
 XX
 XX 23-AUG-2001; 2001GB-00020558.
 PR
 XX 05-OCT-2001; 2001GB-00024037.
 PR
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 PA
 XX Kingeman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 PI WPI; 2003-290046/28.
 XX
 XX N-PSDB; ADD18697.
 DR
 XX
 XX New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.

XX Claim 25; SEQ ID NO 127; 424pp; English.
 XX
 CC This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory,
 CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein of the invention.

XX Sequence 375 AA;
 Query Match 100.0%; Score 1840; DB 7; Length 375;
 Best Local Similarity 100.0%; Pred. No. 5.1e-169;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVNCNFSFPQDWSAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
 DB 20 TTPEPCELDDDFRCVNCNFSFPQDWSAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 79
 QY 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120
 DB 80 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 139
 QY 121 TGLALSSLRNRVSWATGRSMIAELQWLKGLKVLSTAQAHSFAFSYEQVRAFPALTSL 180
 DB 140 TGLALSSLRNRVSWATGRSMIAELQWLKGLKVLSTAQAHSFAFSYEQVRAFPALTSL 199
 QY 181 DLSNDPGLGGERGLMAALCPHFPAQLNLAALNTGNETPTGVCAALAAAGVOPHSLDLGHN 240
 DB 200 DLSNDPGLGGERGLMAALCPHFPAQLNLAALNTGNETPTGVCAALAAAGVOPHSLDLGHN 259
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVDLSCNRLNRAPODEL 300
 DB 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVDLSCNRLNRAPODEL 319

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSCTLLVLLQGARGFA 356
 DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSCTLLVLLQGARGFA 375
 RESULT 4
 AAG68127
 ID AAG68127 standard; protein; 356 AA.
 XX
 XX AAG68127;
 AC
 XX 23-JAN-2002 (first entry)
 DT
 XX Human CD14 amino acid sequence SEQ ID NO:1.
 DE
 XX Human; Toll like receptor; TLR; CD14; antibody; anti-CD14 antibody;
 KW TLR/CD14 binding inhibitor; antibacterial; immunosuppressive;
 KW antipyretic; hypertensive; immunostimulant; haemostatic; vasotropic;
 KW bacterial infection; sepsis; fever; hypotension; leukopaenia;
 KW thrombopaenia; shock; multi-organ failure.

XX Homo sapiens.
 OS
 XX WO200172993-A1.
 XX
 XX 04-OCT-2001.
 PD
 XX 02-APR-2001; 2001WO-JP002869.
 XX
 XX 31-MAR-2000; 2000JP-00099617.
 PR
 XX 22-NOV-2000; 2000JP-00356719.
 PR
 XX 28-MAR-2001; 2001US-00806158.
 PR
 XX (MOCH) MOCHIDA PHARM CO LTD.
 XX
 XX Furusako S, Morii S, Shirakawa K, Takahashi T;
 XX WPI; 2001-616487/71.

XX Anti-CD14 antibody or its fragment inhibiting the binding of CD14 to Toll
 PT -like receptor, applicable in drugs for treating bacterial infection as
 PT well as sepsis, fever, hypotension, leukopenia, thrombopenia and shock.

XX Claim 1; Page 153-155; 202pp; Japanese.

XX The present invention describes an anti-CD14 antibody, which has a
 CC function of inhibiting the binding of CD14 to the Toll-like receptor
 CC (TLR). The anti-CD14 antibody can specifically recognise the epitope
 CC containing the domain from numbers 269-315 in human CD14 of the sequence
 CC in AAG68127 or a part of it. Anti-CD14 antibody has antibacterial,
 CC immunosuppressive, antipyretic, hypertensive, immunostimulant,
 CC haemostatic and vasotropic activities. The antibody together with other
 CC polypeptides are applicable in drugs for treating bacterial infection as
 CC well as sepsis, fever, hypotension, leukopenia, thrombopenia, shock and
 CC multi-organ failure. AAG68127 to AAG68137 and AAI71230 to AAI71295
 CC represent sequences used in the exemplification of the present invention

XX Sequence 356 AA;

Query Match 99.5%; Score 1831; DB 4; Length 356;
 Best Local Similarity 99.7%; Pred. No. 3.5e-168;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVNCNFSFPQDWSAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
 DB 1 TTPEPCELDDDFRCVNCNFSFPQDWSAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
 QY 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120
 DB 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDKITGTMPPLEA 120
 QY 121 TGLALSSLRNRVSWATGRSMIAELQWLKGLKVLSTAQAHSFAFSYEQVRAFPALTSL 180

CC subjects: (a) with CD40 negative or deficient B cells; (b) suffering from
 CC T cell immunodeficiency (e.g. X-linked hyper-IgM syndrome, common
 CC variable immunodeficiency or X-linked agammaglobulinemia) or allergy
 CC (i.e. with CD40 ligand negative or defective T cells); or (c) to induce
 CC growth and differentiation of B cells to highly productive Ig secreting
 CC cells. Particular applications are in infant feeding formulae (as
 CC immunostimulant) and as adjuvant in vaccines (optionally with bovine CD14
 CC coupled to the antigen). The DNA sequences are also used to enrich
 CC mammalian B cells secreting a monoclonal antibody (MAB) of particular
 CC antigenic specificity, by activating cells with sub-optimal amount of the
 CC DNA in combination with the antigen. The enriched B cells are then used
 CC to produce hybridomas that produce specific MAB. Antibodies raised
 CC against human CD14 are used to reduce/inhibit activity of B cells that
 CC are hyperactivated by high serum levels of CD14. Bovine CD14 stimulates
 CC growth (induce DNA synthesis) in resting murine spleen cells and is 200
 CC times more effective than lipopolysaccharide (LPS), with the effect
 CC unaffected by presence of serum. It also induces Ig secretion and a
 CC partial isotype switch from IgM to IgG, in absence of T cells
 XX partial isotype switch from IgM to IgG, in absence of T cells
 SQ Sequence 375 AA;

Query Match 100.0%; Score 1840; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 5.1e-169;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTPECELDDEDFRCVCFNFSEFPQDMSAFQCSAVEVEIHAGGLNLEPFLKRVDDADDP 60
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 20 TTPECELDDEDFRCVCFNFSEFPQDMSAFQCSAVEVEIHAGGLNLEPFLKRVDDADDP 79
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 61 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 80 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 121 TGLALSSLRNLNVSWATGRSWLAELQQLKPLKVLSTIAQHSFAFSYEQVRAFPALTSL 180
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 140 TGLALSSLRNLNVSWATGRSWLAELQQLKPLKVLSTIAQHSFAFSYEQVRAFPALTSL 199
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRLNTGTMETPTGCAALAAAGVOPHSLDLSHN 240
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 200 DLSNPGGLGERGLMAALCPHKFPAIQNALRLNTGTMETPTGCAALAAAGVOPHSLDLSHN 259
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDLP 300
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDLP 319
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLLQGARGFA 356
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLLQGARGFA 375
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
 AAY53878
 ID AAY53878 standard; protein; 375 AA.
 XX AAY53878;
 AC AAY53878;
 XX AAY53878;
 DT 13-MAR-2000 (first entry)
 XX A human CD14 protein which is used to treat sepsis.
 DE CD14; sepsis; epithelial cell; defensin; antibiotic polypeptide; B cell;
 KW infection; immune deficient; wound healing; burn; ulcer;
 KW transgenic animal.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Key
 FT Misc-difference 187
 FT /note= "encoded by TGC"
 XX WO9961468-A2.
 PN 02-DEC-1999.
 PD

XX 27-MAY-1999; 99WO-CA000482.
 PF 27-MAY-1998; 98US-0086884P.
 PR (GEMM-) GEMMA BIOTECHNOLOGY LTD.
 XX Julius MH, Philipp D;
 XX WPI; 2000-072604/06.
 DR N-PSDB; AAZ36819.
 XX Treating sepsis and activating B cells by administration of soluble CD14,
 PT e.g. for preventing infection.
 PS Claim 10; Page 56-58; 61pp; English.
 XX The present sequence represents a CD14 protein. The protein is used in
 CC the method of the invention. The specification describes a method whereby
 CC symptoms of sepsis are ameliorated by exposing epithelial cells in a
 CC mammal directly to soluble CD14 or its fragments. The CD14 is capable of
 CC stimulating expression of a defensin by the epithelial cells. CD14
 CC directly induces expression of antibiotic polypeptides, specifically
 CC defensins, in mammals and stimulates B cells (i.e. induces
 CC differentiation of their precursors). CD14 protein is used to treat
 CC sepsis; to stimulate B cells, particularly for protection against
 CC infection (viral, bacterial, fungal or yeast), especially in immune
 CC deficient subjects, and to promote healing of wounds (burns, ulcers).
 CC Transgenic animals containing exogenous sequences encoding CD14 are used
 CC for enhanced production of CD14 in the milk
 XX Sequence 375 AA;

Query Match 100.0%; Score 1840; DB 3; Length 375;
 Best Local Similarity 100.0%; Pred. No. 5.1e-169;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTPECELDDEDFRCVCFNFSEFPQDMSAFQCSAVEVEIHAGGLNLEPFLKRVDDADDP 60
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 20 TTPECELDDEDFRCVCFNFSEFPQDMSAFQCSAVEVEIHAGGLNLEPFLKRVDDADDP 79
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 61 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 80 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 121 TGLALSSLRNLNVSWATGRSWLAELQQLKPLKVLSTIAQHSFAFSYEQVRAFPALTSL 180
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 140 TGLALSSLRNLNVSWATGRSWLAELQQLKPLKVLSTIAQHSFAFSYEQVRAFPALTSL 199
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRLNTGTMETPTGCAALAAAGVOPHSLDLSHN 240
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 200 DLSNPGGLGERGLMAALCPHKFPAIQNALRLNTGTMETPTGCAALAAAGVOPHSLDLSHN 259
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDLP 300
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDLP 319
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLLQGARGFA 356
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLLQGARGFA 375
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
 ADD18696
 ID ADD18696 standard; protein; 375 AA.
 XX ADD18696;
 AC ADD18696;
 XX ADD18696;
 DT 15-JAN-2004 (first entry)
 XX Human disease related protein SeqID127.
 DE Human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW human; disease state; cytostatic; antiinflammatory; ophthalmological;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 126 Seconds
(without alignments)
798.309 Million cell updates/sec

Title: US-09-807-709D-1
Perfect score: 1840
Sequence: 1 TTPPCLEDDERFCVNF.....TLISGVSGTILVLQARGFA 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1930s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1840	100.0	375	2 AAW60854	Human CD1
2	1840	100.0	375	3 AAY53878	A human C
3	1840	100.0	375	7 ADD18696	Human dis
4	1831	99.5	356	4 AAG68127	Human CD1
5	1831	99.5	356	4 AAB73984	Human sol
6	1831	99.5	375	2 AAW05316	Myelomono
7	1831	99.5	375	4 AAG68129	Human CD1
8	1831	99.5	375	5 ABB83163	Human CD1
9	1831	99.5	375	7 ADD25617	Binding d
10	1831	99.5	375	7 ADE55388	Human Pro
11	1831	99.5	375	7 ADD89019	TAT258. 1
12	1827	99.3	356	5 AAO22313	Anti-CD14
13	1826	99.2	375	2 AAW41693	Human CD1
14	1807	98.2	431	3 AAB58147	Lung canc
15	1791	97.3	348	2 AAR98576	CD14 sequ
16	1766	96.0	348	2 AAW00467	Soluble C
17	1764	95.9	348	2 AAW00469	Soluble C
18	1764	95.9	348	2 AAW00473	Soluble C
19	1763	95.8	348	2 AAW00470	Soluble C
20	1763	95.8	348	2 AAW00472	Soluble C
21	1763	95.8	348	2 AAW00471	Soluble C
22	1762	95.8	348	2 AAW00468	Soluble C
23	1633	88.8	339	7 ADD29966	Human mod
24	1611	87.6	318	2 AAW00474	Soluble C
25	1577	85.7	307	4 AAG68131	TLR/CD14

ALIGNMENTS

RESULT 1

AAW60854
ID AAW60854 standard; protein; 375 AA.

XX AAW60854;

XX 01-OCT-1998 (first entry)

XX Human CD14 protein.

XX CD14; B cell activator; bovine lactation-associated immunotropic protein;

XX LAIT; T cell immunodeficiency; X-linked hyper-IgM syndrome; allergy;

XX common variable immunodeficiency; X-linked agammaglobulinaemia; vaccine;

XX infant feeding formulae; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Key Misc-difference 87 /note= "encoded by TGC"

XX WO9822580-A2.

XX 28-MAY-1998.

XX 18-NOV-1997; 97WO-CA000880.

XX 18-NOV-1996; 96US-00746883.

XX (WELL-) WELLESLEY HOSPITAL FOUND.

XX Julius MH, Philipp D, Alizadeh-Khiavi K;

XX WPI; 1998-312466/27.

XX N-ESDB; AAV37228.

XX New bovine polypeptide that activates mammalian B cell(s) - used e.g. to treat T cell immunodeficiency or allergy, as vaccine adjuvant, as T cell surrogate for infants, and for monoclonal antibody production, also specific antibodies for treating B cell hyperactivity.

XX Claim 14; Fig 7; 64pp; English.

XX This sequence is the human CD14 protein of the invention. The CD14

XX protein was used to isolate the bovine CD14 of the invention, which is

XX able to activate mammalian B cells. The protein is also known as bovine

XX lactation-associated immunotropic protein (LAIT), and is used to activate

XX B cells, particularly in humans. Particularly it is administered to

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```
Qy 73 RRLTVGAQVPAQLLVGALRVLAYSRILKELTLEDKITGTMPPLPLEATGLALSSLRIN 132
Db 81 RRTRIG-NQNP-EFVGSL--VNLRASFNASRFYLPGFIPAL----- 120
Qy 133 VSWATGRSLAELQQLWKLKPGIKVLSIAQAHSFAPSYEQVRAFPALTSLDLSDNFGLG 192
Db 121 ----FGSLLT-----LEVLDLSSCSITGTIPESLTRLSHLKVLDSLKNAINGD-- 165
Qy 193 LMAALCPHKFPATQNLALRNTGTMETPTGVCALAAAGVQHSLDLSDNLRATVNPAPR 252
Db 166 ----IPLSLTSLQNLGILDSSNVFSGIPANIGALSKLQRLNLSRNLTLTSSIPPSLGD 220
Qy 253 CMWSSALNSLSPAGLE-QVP---KGLPAKLRLVLDLSCNRLNRAPOPD----- 297
Db 221 L---SVLIDLDLSPNGSGSVPSOLKGL-RNLQTLVIAGNRLSGSLPPDLFSLLSKLQII 276
Qy 298 -----ELPEVDNLTLDGNPF--LVPGTALPHEGSMN 326
Db 277 DFRGSGFIALPSRLMSLPKFLDISGNHFSMDLNPNTVTSFSDSTVS 323

RESULT 15
D84434
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84434
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84434
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1008 <SIO>
A:Cross-references: GB:AE002093; NID:96598459; PIDN:AACT8507.2; GSPDB:GN00139
C:Genetics:
A:Gene: At2g02220
A:Map position: 2

Query Match 6.5%; Score 120.5; DB 2; Length 1008;
Best Local Similarity 25.2%; Pred. No. 0.2;
Matches 67; Conservative 36; Mismatches 72; Indels 91; Gaps 16;

Qy 94 LAYSRLKELTLEDKITGTMPPLPLEATGLALSS---LRLRNVSW--ATGR--SWLAEIQ 146
Db 412 LHFEEKLVLVVANCRLTGSMPRW-----LSSSNEQLQLDLSDNRLTGAIPSWIGD-- 461
Qy 147 QWLKPGKLKLSIAQAHSFAPSYEQVRAFPALTSLDLSDNFGLGRLMAALCPHKFPAIQ 206
Db 462 -----FKALFYLDLSNNSFTGE-----IPKSLTKLE 487
Qy 207 NLALRNTGMEPTG-----VCAALAAAGVQ-----PHSLDLSDNLRATVNPAPRCM 254
Db 488 SLTGRNISVNEPSPDPFFPMKRNESARALQYNQIFGFPPTIELGHNNL-----SGP--I 539
Qy 255 WS-----SALNSLNSFAGLE-QVPKGLP--AKLRLVLDLSCNRLNRAFPQDPDELPEVDNLT 306
Db 540 WEEFGNKKLVHFDLKNALSGSIPSSLSGMTSLEALDLSNNRLS-GSIPVSLQQLSFL- 597
Qy 307 LDGNPFLVPGTALPHEGSMNSGVPA 332
Db 598 ---SKFSVAYNNL-----SGVIPS 613
```

Search completed: October 4, 2004, 16:54:20
Job time : 46 secs

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C:Accession: S42799; I37407

R:Birnbaum, D.

submitted to the EMBL Data Library, July 1993

A:Reference number: S42799

A:Accession: S42799

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-662 <R>

R:Ollendorff, V.; Noguchi, T.; deLapeyriere, O.; Birnbaum, D.

Cell Growth Differ. 5, 213-219, 1994

A:Title: The GARP gene encodes a new member of the family of leucine-rich repeat-contain

A:Reference number: I37407; MUID:94235567; PMID:8180135

A:Accession: I37407

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-662 <RES>

A:Cross-references: EMBL:224680; NID:G4392295; PIDN:CAA80847.1; PID:G439296

C:Genetics:

A:Gene: GDB:GARP; D118833E

A:Cross-references: GDB:433911

A:Map position: 11q13.5-11q14

C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

F:50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F:150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F:244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F:266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F:316-339/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>

F:340-363/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>

F:364-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>

F:411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>

F:444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>

F:467-490/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>

F:492-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>

F:515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

F:537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR20>

Query Match 6.7%; Score 124; DB 2; Length 662;

Best Local Similarity 26.1%; Pred. No. 0.06;

Matches 84; Conservative 38; Mismatches 90; Indels 110; Gaps 17;

QY 75 LTVGAA-----QVFAQLLVGALRVLAYSRKLELTLEDLKITGTMPPLEATGLAISLR 129

DB 12 LTLGLAAHQDKVPCMYD-----KXVSCQVGLLQVPSVLPDPDTETDLSGNQ 60

QY 130 LRVSWATGRSWLAELQ-----QWLKPG-----LKVLSAQ---AHSFAPSYEQ 170

DB 61 LRS1-LASPLGFYTLARHLDTSTNEISFLOPQAFQALTHLEHLSLAHRLAMATLSAGG 119

QY 171 VRAPPALTSLSLSDN---PGLGERGLMAALCPHKEPAIQNAL-----RNTGMEPT 218

DB 120 LGPLPRVTSLSLSDNSLSYGLLERLLGEA-----PSLHTLSLAENSUTRTRHTRFDM 173

QY 219 TGVCAALAAAGVQPHSLDLSHNSLRATVNPISA---PRCMSSALNSLNFAGLEQVPK 274

DB 174 -----AL-----EQDL-LHSNVLMQIEDGAFGLPR-----LTHLSLNSLTCISD 214

QY 275 GLPAKLRVLDLSNRL---NRAPQD-----ELPEVDNLTLDG 309

DB 215 FSLQQLRVLDLSNCSIEAFATSQPQABFQLTWLDRNKLLHFPDLAALPRLLIYLNLSN 274

QY 310 NPELVP-----GTALPHSG 323

DB 275 NLRLP'GPPQDSKGIHAPSEG 296

RESULT 13

JC5239

insulin-like growth factor acid-labile chain - baboon

C:Species: Papio sp. (baboon)

C>Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997

C:Accession: JC5239

R:Delhanty, P.; Baxter, R.C.

Biotech. Biophys. Res. Commun. 227, 897-902, 1996

A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like

A:Reference number: JC5239; MUID:97040714; PMID:8886027

A:Contents: liver

A:Accession: JC5239

A:Molecule type: mRNA

A:Residues: 1-605

C:Comment: This factor is structurally related to proinsulin and have insuline-like metal

Query Match

Best Local Similarity 6.7%; Score 122.5; DB 2; Length 605;

Matches 103; Conservative 51; Mismatches 158; Indels 99; Gaps 22;

QY 8 LDEDFRCVCFSEFPQDWSE-----AFQCVSAVEVEIHAGG--LNLEPFLKRVADA 58

DB 161 LEDGLFEGLGNLWDLNLCWNSLAVLPDAAFRGGLGRLVLAGNRLAYLQPAL--FSGLA 218

QY 59 DPRQYADTVKALRVRLTVGAAQVPA-----QLLVGALRVLAYSRUKELTLEDL---K 108

DB 219 ELRELDLSRNALRAIKANV-FAQLPRLOKYLDRNLAAVAPGAPGLKALRWLDLSNR 277

QY 109 ITG---TMPPL---PLEATGLALSRLRNV-----SWATGRSWLAELQWLKPKGL 153

DB 278 VAGLEDTFPGLLGLRVLRSHNAISLRPTFEDLHLELQGHNNRIOLAERSFGL 337

QY 154 KVLISIAQHSFAPSYEQVRAFPALTS---LDSLSDN-----PGLG-----ERGL 193

DB 338 GQLEVLTDHNLQLEVKVGFGLTNVAVMLSGNCLRNLPQEVFRGLKLSHLEGGC 397

QY 194 MAALCPHKF---PAIQNALRNTGM-----ETPTGVCAALAAAGVQ-----PHSLD--- 236

DB 398 LGRIPTHFAGLSGLRLFLKDNGLVGTIEQSLMGLAELELDELTSNQLTHLPQOLFOGL 457

QY 237 -----LSHN---SLRATVNPSPRCMSSALNSLNFAGLEQVPKLPA---KLRLV 283

DB 458 GKLEVLILLSHNRLEALPADALGPQRAFV-----LOVSHNRLEALPQSLASGLRLYL 511

QY 284 DLSNLRNR-APQDELPEDVNLTLDGNNPF--LVPGTALPHEGSMNSGVWP 331

DB 512 NLNRNSLRITFTFQP---PGLERLWLEGNPMDSCPLKALRDFALQNPSAVP 559

RESULT 14

T08575

protein kinase homolog T22F8.170 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 17-Mar-2000

C:Accession: T08575

R:Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Maye

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16442

A:Accession: T08575

A:Molecule type: DNA

A:Residues: 1-864 <BEV>

A:Cross-references: EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.170

A:Experimental source: cultivar Columbia; BAC clone T22F8

C:Genetics:

A:Gene: ATSP:T22F8.170

A:Map position: 4

A:Introns: 632/2; 675/2; 683/1

C:Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology; p

Query Match

Best Local Similarity 6.6%; Score 121.5; DB 2; Length 864;

Matches 69; Conservative 40; Mismatches 101; Indels 77; Gaps 12;

A:Gene: At2g27060
A:Map position: 2

Query Match 7.4%; Score 136.5; DB 2; Length 1007;
Best Local Similarity 22.8%; Pred. No. 0.01;
Matches 85; Conservative 53; Mismatches 131; Indels 103; Gaps 18;

QY 49 PFLKRVDA-DADPRQYADTV-----KALVRRLTVGAQVPAQL----- 86
DB 226 PFDLSLEVPDASSNQLSGSVFVSFKILRLQDNQLSASLPGLQESITLTDLDL 285
QY 87 ----LVGALRVLAYSRLELTLEDTGTMTGTPLEATGALSSILRLNRSWATGRSML 142
DB 286 SINQLEGPISGTSITSLKINLSSNLSGS---LPLKVGHCAIIDLNNKIS-----GEL 337
QY 143 AELQW-----LKPQ-----LKVLSIAQAHPAFSYEQVRAF-----PA 176
DB 338 SRIQWGDVSVEIRLSSNSLTGLPQTSQFRLTSLKAANN---SLQCVLPFILGTYPE 394
QY 177 LTSLDSDNPGGLGERGLMAALCPHF---PAIQNALRNTGNETGTGVCALAAAGVQPH 233
DB 395 LXEIDLSNQ-----LSGVPSNLFISAKITELNLSNNFSGSLPQDASTVGNLSLT 447
QY 234 SLDSLSLRATVNPSPAPRCMWSALNSLSFAGLE-QVPKGLPAKLRVLDLSCNRLNR 292
DB 448 NIGLSHSLGGVLSLELTR---FHNLSLDSLYNNFEGNIPDGLPDSLKMTFTVSANNLS- 503
QY 293 APQDELPE-----VDNLTLDGNPFLVPGTALP-----HSGMSNGSVVPACARST 337
DB 504 ----GNVPENLRFPDSAFHGNALLNVPISLPKDKTITLRKHGHHKTSV-----KAA 554
QY 338 LSVG-VSGTLVL 348
DB 555 LIIGLVGTALL 566

RESULT 7
AG0123
Probable antigenic leucine-rich repeat protein YPO1007 [imported] - Yersinia pestis (strain AG0123)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AG0123
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A.; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0123
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-605 <KUP>
A:Cross-references: GB:AL590842; PIDN:CAC09850.1; PID:gl5979076; GSPDB:GN00175
C:Genetics:
A:Gene: YPO1007

Query Match 7.2%; Score 132; DB 2; Length 605;
Best Local Similarity 23.6%; Pred. No. 0.012;
Matches 69; Conservative 41; Mismatches 78; Indels 104; Gaps 14;

QY 76 TVGAQVPA-----QLLVGALRVLAYSRLE-----LTLEDKITG--- 111
DB 26 TSTAALTADYAIWEKWNEDPRIVAGQORQAVRMKECLENTERTLDELGLTSLPD 85
QY 112 TMPPLEATGALSSLRNRSWATGRSWLAELQOMLKPGLKVLSTIAQAHPAFSYEQV 171
DB 86 TLPPCN-----KLNII---ENKLTLPPTLPDNLQTLNAA-----ENQL 121
QY 172 RAFF-----ALTSILSDNPGGLGERGLMAALCPHFPA- 204
DB 122 RTLNTLTPASLLSNVYGNELERLPELSPEGLKKLDVGRNESLQ-----PNRLPPN 173
QY 205 IQNALRNTGM-ETPTGVCAALAAAGVQPHS---LDLSHNSLRATVNPSPAPRCMWSALN 260

DB 174 LESLGMANCRLELTPT-----LPNSLEKLEVDNNQLH-TLPDTLP-----ALIS 216

QY 261 SINLSFAGLEQVPKGLPAKLRVLDLSCNLRNAPQDELPEVDNLTLDGNPF 312
DB 217 SLIVSSNRLTALPENLPQSLRDIVAKDNQLSQLPDLAHLPONCSRILDGNPF 268

RESULT 8
TI0636

Hypothetical protein T13K14.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999

C:Accession: TI0636

R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke,

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16991

A:Accession: TI0636

A:Molecule type: DNA

A:Residues: 1-1143 <BEV>

A:Cross-references: EMBL:AL080282; GSPDB:GN00062; ATSP:T13K14.100

A:Experimental source: cultivar Columbia; BAC clone T13K14

C:Genetics:

A:Gene: ATSP:T13K14.100

A:Map position: 4

A:Introns: 334/1; 815/2; 941/3; 970/2; 1006/3; 1031/1; 1073/3; 1105/3

Query Match

Best Local Similarity 7.0%; Score 129; DB 2; Length 1143;

Matches 93; Conservative 24.0%; Pred. No. 0.049;

Mismatches 93; Indels 138; Gaps 19;

QY 30 POCVSAVEV-BIHA-----GGUNLEPFL-----KRYDADADPRQYADTVKAL-----RVRL 75

DB 194 FELISSLEVLHDGNSIDGNLDGEFFLLTNASYVDISN-RLVTTSGKLLPGVSESIRHL 252

QY 76 TVGAQVPAQLLVG-----ALRVLAIS-----RLKELTLEDKITGTMP 115

DB 253 NLSHNLQSGTSFGFQFNKLKVLDSYNNLSGELPGFNYYVDLEVLKSNRFSGLPN 312

QY 116 LPLEATGLALSRL--RNVSWATGRSWLAELQOMLKPGLKVLSTIAQAHPAFSYEQVRA 173

DB 313 NLLKGSLLTLTLDLSGNLS-----GVSIMS----- 341

QY 174 PPAITLSDNPGGLGERGLMAALCPHFPAIQNALRNTGNETGTGVCALAAAGVQPH 233

DB 342 -TTLTLDLSSNSLTGELPL-----TGCVLLDLSNNQPE 376

QY 234 S-----LDLSHNSLRATVNPSPAPRCMWSALNSLSFAGL-----EQVPG 275

DB 377 GNLTRWSKNWENIEYLDLSQNHFTGSPDPTPOLL---RANHLNLSYNNKLTGSLPERIPT 433

QY 276 LPKLRVLDLSCNLRNAPQDEL---PEVDNLTLDGNPFLVPGTALPHGS----- 324

DB 434 YP-KLRVLDISSNSL-EGPIPGALLSMPTLEEHLQNNGMTGNIGLPSSGSRIRLLDLS 491

QY 325 --MNSGVVPACARSTLSVGSGTLVLQ 350

DB 492 HNRFDGDL-----GVFGSLTNLQ 510

RESULT 9

AF0123

Probable antigenic leucine-rich repeat protein YPO1006 [imported] - Yersinia pestis (strain AG0123)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: AF0123

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A.; Title: Genome sequence of Yersinia pestis, the causative agent of plague.

Nature 413, 523-527, 2001

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AF0123

F;266-288/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;497-830/Domain: gelsolin repeat homology <GEL1>
F;892-1250/Domain: gelsolin repeat homology <GEL2>

```
Query Match      8.2%; Score 150.5; DB 2; Length 1256;
Best Local Similarity 23.0%; Pred. No. 0.0011;
Matches 92; Conservative 48; Mismatches 103; Indels 157; Gaps 18;

QY 45 LNLPEFLKRVDAAD--PROVADTVKAL-RVRRLTVG---AAQVPAQI----- 86
Db 1 MSVLFFVRGVDFTKNDFSATFPSSMRQMSRVQWLTDLTQLAETPEELHQLKLEHLSLN 60
QY 87 -----LVGALRVLAYSLKELTLEDKITGTMPPL--PLEATGLALSSLRLRNVSWATG 138
Db 61 HNRLEKIFGELTELSCURSDLRHQNQKNGSIPPELFHLELTITLDLSHNKLKXEVPEGLE 120
QY 139 RSMIAELQWLKPKGLKVLIAQAH-----SPAF-----SYBQVRAFFA----- 176
Db 121 RA-----KNLIVNLNNQIESIPTPLFTHLTDLFLDLSHNRLETLPQTTRLI 170
QY 177 -LTSLDLSDNPGIGERGMAALCPHKFPAIONLAL-----RNTGMEPTGVCVCAALAAAG 229
Db 171 NLKTLDSLHNP-----LELFQRLPSLQSLVLEVKSGTQRTLLNFPPTSIDSLANLC- 222
QY 230 VQPHSLDLSHNSLRATVNSAPRCMWS-----SALNSLNL 265
Db 223 -----ELDSLHNSL-----PKLPDCVYVTVLRLNLSDELTELTAGVELWQRLSLS 273
QY 266 -----FAG-----LEQVPKGL- 276
Db 274 RNQVALPAALCKLPKRLRLVNDNKNFEGIPSGIGKGLGALEVFSANLLEVMVEGLC 333
QY 277 -PAKLRVLDSLNRNAPQDELPE-VDNLTLDGNPLV 314
Db 334 RCGALKQLNSCNRLITLPDAIHLEGLDQLDLRNNPELV 373

*
RESULT 4
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C;Accession: T08664
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16466
A;Accession: T08664
A;Molecule type: mRNA
A;Residues: 1-786 <POU>
A;Cross-references: EMBL:AL050262
A;Experimental source: fetal brain; clone DKFZp547I0610
C;Genetics:
A;Note: DKFZp547I0610.1
```

```
Query Match      7.9%; Score 145; DB 2; Length 786;
Best Local Similarity 24.9%; Pred. No. 0.0016;
Matches 71; Conservative 39; Mismatches 115; Indels 60; Gaps 10;

QY 94 LAYSLKELTLEDKITGTMPPLPEATGLALSLRLNRNVSWATGRSWLAELQ----- 146
Db 216 LELSNIK-CVLEDSKCVFLSLAKLTQNPKLSSLTNNIE-TTWSPIRILQLVWHTV 273
QY 147 -----QWLKGLKVLSTQAHSAPSPSYEQVRAFPALTSLDLSNPG 187
Db 274 WYSSISNVKQGQDLDFRDFSGTSLKALSILHQVVDVFGPPQSYIIFSNMKNKPTV 333
QY 188 LGERGLMAALCPHKFPAIONLALRN-----TGME-----PTGVCAA 224
Db 334 SGTR-MVHMLCPKSLPPLHLDFSNLLTDTVFENCGLHTELETLLQMNQKLSKIAE 392
QY 225 LAAAGVQPHSLDLSHNSLRATVNSAPRCMWSALNSLNSFAGL-EQVPKGLPAKLRVL 283
Db 393 MTTQMKSLQQLDISQNSV--SYDEKKGDCSWTKSLLSLNMSNLTITDIFRCLPPIKVL 450
```

```
QY 284 DLSCNRLNRP-OPDELPEVDNLTLDGNPFLVPGTALPHEGSMNS 327
Db 451 DLHSNKIKSIKQVVKLEALQELNVAENSL-----TDLPGCGSFSS 491

RESULT 5
T48499
receptor-like protein kinase-like protein - Arabidopsis thaliana
N;Alternate names: protein T28J14.220
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T48499
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24493
A;Accession: T48499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1192 <BEV>
A;Cross-references: EMBL:AL163652
A;Experimental source: cultivar Columbia; BAC clone T28J14
C;Genetics:
A;Map position: 5
A;Note: T28J14.220

Query Match      7.7%; Score 142; DB 2; Length 1192;
Best Local Similarity 23.9%; Pred. No. 0.0047;
Matches 83; Conservative 48; Mismatches 116; Indels 100; Gaps 14;

QY 77 VGAQVPAQLLVGAL--RVLAYSLKELTLEDKITGTMP-----LPLEATGLALS 126
Db 67 VNSLSLPSLSLRGQIPKEISSLKRLRELCLAGNFGSKIPPEIWNKHLQLTDLSGNSLT 126
QY 127 SLRLNVSWATGRSWLAELQWLKVLIAQAHSPAPSYEQVRAFPALTSLDLSNPG 186
Db 127 GLLP-----LLSELQQLYLDLSDNHFSGSLPSPFI-----SLPALSSLDVSNNS 173
QY 187 GLGERGLMAALCPHKFPAIONLALRNTGMEPTG-----VCAALAAA-----GVQ 231
Db 174 LSGR-----IPPEIKLSNLSNLYMGLNSFSGQIPSEIGNISLLKNFAAPSCFFNGPL 226
QY 232 PH-----SLLDLSHNSLRATVNSAPRCMWSALNSLNSFAGLEQVPKGLPAKLRV 282
Db 227 PKEISKLKLAKLDLSYNPLKCSIPKSGELHNLILNLVSAELIGLIPPELGNCKSLKS 286
QY 283 LDLSNRLNRPQDELPEV-----DNLTLDGNPFLVPG 316
Db 287 LMLSFNLSL-GPLPLELSEIPLLTFSARNQLSGSLPSWMGKWKVLDLSSLLANNRF---S 342
QY 317 TALPHE-----GSMNSGVVP--ACARSTL-SVGVSGTLV 347
Db 343 GEIPHEIEDCPMLKHLSLASNLSSGSLPRLCGSGSLAIDLGNLL 389

RESULT 6
C84668
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84668
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:1061197
A;Accession: C84668
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1007 <STO>
A;Cross-references: GB:A8002093; NID:G3885336; PIDN:AAC77864.1; GSPDB:GNC00139
C;Genetics:
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A:Gene: GDB:CD14
A:Cross-references: GDB:119759; OMIM:158120
A:Map position: 5q31.1-5q31.1
A:Introns: 1/3
C:Superfamily: monocyte surface glycoprotein CD14
C:Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-375/Product: monocyte surface glycoprotein CD14 #status predicted <MAT>
F:20-367/Product: monocyte surface glycoprotein CD14 #status predicted <MAT>
F:91-329/Region: 9-residue repeats (LV)-X-X-L-X-[LV]-[SRTA]-X-[NAT]
F:37,151,282,323/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 1840; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-139;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTPPECELDDEDFRCVNFSEPPQDMSFAQCVAVEIHAAGGLNLEPFLKRVDAADP 60
DB 20 TTPPECELDDEDFRCVNFSEPPQDMSFAQCVAVEIHAAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLEA 120
DB 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLEA 139
QY 121 TGLALSSRLRNVSATGRSWLAELQQLKPKGLKVLISIAQAHSFAFSYEQVRAFPALTS 180
DB 140 TGLALSSRLRNVSATGRSWLAELQQLKPKGLKVLISIAQAHSFAFSYEQVRAFPALTS 199
QY 181 DLSNPGLGERGLMAALCPHKFPATQNLALRNTGTTGVCALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGLGERGLMAALCPHKFPATQNLALRNTGTTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNSAPRCMWSALNSLNFAGLEQVPGKLPKLVLDLSCNRLNRAPODEL 300
DB 260 SLRATVNSAPRCMWSALNSLNFAGLEQVPGKLPKLVLDLSCNRLNRAPODEL 319
QY 301 EVDNLTLDGNPFLVGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGF 356
DB 320 EVDNLTLDGNPFLVGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGF 375
RESULT 2
TDM54
monocyte surface glycoprotein CD14 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 16-Jun-2000
C:Accession: S03605; A43539; S04967
F:Matsumura, K.; Setoguchi, M.; Nasu, N.; Higuchi, Y.; Yoshida, S.; Yamamoto, S.
Nucleic Acids Res. 17, 2132, 1989
A:Title: Nucleotide and amino acid sequences of the mouse CD14 gene.
A:Reference number: S03605; MUID:89183627; PMID:2467257
A:Accession: S03605
A:Molecule type: DNA
A:Residues: 1-366 <MATS>
A:Cross-references: EMBL:X13987; NID:G50336; PIDN:CAA32166.1; PID:G2342527
F:Ferrero, E.; Hsieh, C.L.; Francke, U.; Goyert, S.M.
J. Immunol. 145, 331-336, 1990
A:Title: CD14 is a member of the family of leucine-rich proteins and is encoded by a gene
A:Reference number: A43539; MUID:90293480; PMID:1694207
A:Accession: A43539
A:Molecule type: DNA
A:Residues: 1-366 <FER>
A:Cross-references: GB:M34510; NID:G192460; PIDN:AAA37387.1; PID:G387121
F:Setoguchi, M.; Nasu, N.; Yoshida, S.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.
Biochim. Biophys. Acta 1008, 213-222, 1989
A:Title: Mouse and human CD14 (myeloid cell-specific leucine-rich glycoprotein) primary
A:Reference number: S04967; MUID:89287330; PMID:2472171
A:Accession: S04967
A:Molecule type: mRNA
A:Residues: 1-366 <SET>
A:Cross-references: EMBL:X13333; NID:G50338; PIDN:CAA31710.1; PID:G50339
C:Genetics:

A:Introns: 1/3
C:Superfamily: monocyte surface glycoprotein CD14
C:Keywords: glycoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
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F:87-323/Region: 9-residue repeats (LV)-X-X-L-X-[LV]-[SRTA]-X-[NAT]
F:33,147,180,276,317/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 61.8%; Score 1136.5; DB 1; Length 366;
Best Local Similarity 65.7%; Pred. No. 6.2e-83;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;
QY 3 PEPCELDDEDFRCVNFSEPPQDMSFAQCVAVEIHAAGGLNLEPFLKRVDAADP 62
DB 20 PEPCELDDEES--CSCNFSDDPKPDMSSAFNCLGAADVLYGGGSRLEYLLKRVDTADLQG 77
QY 63 YADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLEA 122
DB 78 FTDIYKLSLRLTVRAARIFSRILFGALRVLGISGLQELTLENLEVTGTAPPPLEA 137
QY 123 LALSRLRNVSATGRSWLAELQQLKPKGLKVLISIAQAHSFAFSYEQVRAFPALTS 182
DB 138 PDNLNLRNVSWATRDALAEQLQQLKPKGLKVLISIAQAHSFAFSYEQVRAFPALTS 197
QY 183 SDNPGLGERGLMAALCPHKFPATQNLALRNTGTTGVCALAAAGVQPHSLDLSHN 242
DB 198 SDNPGLGERGLISALCPKFPATQNLALRNTGTTGVCALAAAGVQPHSLDLSHN 257
QY 243 RATVNSAPRCMWSALNSLNFAGLEQVPGKLPKLVLDLSCNRLNRAPODEL 302
DB 258 RDA--GAPSCDWSQLNSLNFAGLEQVPGKLPKLVLDLSCNRLNRAPODEL 315
QY 303 DNLTDGNPFLVGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGF 355
DB 316 GNLILKGNPFL---DSHSEKFNKSVGTAGAPSSQVALSGTLALLGDLRF 365
RESULT 3
S60461
gene flightless-I protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: S60461; T08425
F:de Couet, H.G.; Fong, K.S.K.; Weeds, A.G.; McLaughlin, P.J.; Miklos, G.L.G.
Genetics 141, 1049-1059, 1995
A:Title: Molecular and mutational analysis of a Gelsolin-family member encoded by the fly
A:Reference number: S60461; MUID:96129280; PMID:8582612
A:Accession: S60461
A:Molecule type: DNA
A:Residues: 1-1256 <DEC>
A:Cross-references: GB:AF017777; EMBL:U28044; NID:G3004652; PIDN:AAC28407.1; PID:G3004661
F:Maleszka, R.; de Couet, H.G.; Miklos, G.L.
Proc. Natl. Acad. Sci. U.S.A. 95, 3731-3736, 1998
A:Title: Data transferability from model organisms to human beings: insights from the fur
A:Reference number: Z16415; MUID:98188272; PMID:9520435
A:Accession: T08425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1256 <NAL>
A:Cross-references: GB:AF017777; GB:U080043; GB:U28044; NID:G3004652; PIDN:AAC28407.1; PID:
C:Genetics:
A:Gene: fli-I; flightless-I
A:Cross-references: FlyBase:FBgn0000709
A:Introns: 18/3; 1070/2; 1120/3
F:53-75/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:76-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:101-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:124-147/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:148-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:171-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:220-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:243-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 41 Seconds
(without alignments)

835.224 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTPPCLEDDERFCVNF.....TLGVGVGTLVLQARGFA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: Piri:*

2: Piri2:*

3: Piri3:*

4: Piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1840	100.0	375	1 TDHUM4	monocyte surface g
2	1136.5	61.8	366	1 TDMSN4	monocyte surface g
3	150.5	8.2	1256	2 S60461	gene flightless-1
4	145	7.9	786	2 TC8664	Toll protein-like
5	142	7.7	1192	2 T48499	receptor-like prot
6	136.5	7.4	1007	2 C84668	probable receptor-
7	132	7.2	605	2 AG0123	probable antigenic
8	129	7.0	1143	2 T10636	hypothetical prote
9	128	7.0	291	2 AF0123	probable antigenic
10	127.5	6.9	905	2 T00475	probable disease r
11	126.5	6.9	1196	2 T09356	brassinosteroid-in
12	124	6.7	662	2 S42799	grass precursor - h
13	122.5	6.7	605	2 JC5239	insulin-like growt
14	121.5	6.6	864	2 T08575	protein kinase hom
15	120.5	6.5	1008	2 D84434	probable receptor-
16	119	6.5	626	2 AB0123	probable antigenic
17	119	6.5	835	2 T05259	probable disease r
18	119	6.5	890	2 T00800	disease resistance
19	117.5	6.4	858	2 T00258	hypothetical prote
20	117	6.4	987	2 TS0850	receptor protein k
21	115.5	6.3	1068	2 H96769	hypothetical prote
22	115	6.2	788	2 AG0786	secreted effector
23	114.5	6.2	1112	2 T10504	disease resistance
24	113	6.1	462	2 D84858	hypothetical prote
25	113	6.1	981	2 TS0851	receptor protein k
26	113	6.1	1134	2 T04587	hypothetical prote
27	112.5	6.1	960	2 G84652	probable receptor-
28	112.5	6.1	1389	2 T13852	gene wheeler prote
29	112	6.1	768	2 T17462	disease resistance

ALIGNMENTS

RESULT 1

TDHUM4

monocyte surface glycoprotein CD14 precursor - human

N;Alternate names: monocyte differentiation antigen CD14;

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 22-Jun-1999

C;Accession: A27637; S00917; S04968; PLO108; A30555

R;Haziot, A.; Chen, S.; Ferrero, E.; Low, M.G.; Silber, R.; Goyert, S.M.

J. Immunol. 141, 547-552, 1988

A;Title: The monocyte differentiation antigen, CD14, is anchored to the cell membrane b

A;Reference number: A27637; MUID:88258060; PMID:3385210

A;Accession: A27637

A;Molecule type: mRNA

A;Residues: 1-375 <HAZ>

R;Ferrero, E.; Goyert, S.M.

Nucleic Acids Res. 16, 4173, 1988

A;Title: Nucleotide sequence of the gene encoding the monocyte differentiation antigen,

A;Reference number: S00917; MUID:88234022; PMID:2453848

A;Accession: S00917

A;Molecule type: DNA

A;Residues: 1-375 <FBR>

A;Cross-references: EMBL:X06882; NID:g29736; PIDN:CAA29999.1; PID:g312399

R;Setoguchi, M.; Nasu, N.; Yoshida, S.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.

Biochim. Biophys. Acta 1008, 213-222, 1989

A;Title: Mouse and human CD14 [myeloid cell-specific leucine-rich glycoprotein] primary

A;Reference number: S04967; MUID:89287330; PMID:2472171

A;Accession: S04968

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-186 'C', 188-375 <SET>

A;Cross-references: EMBL:X13334; NID:g29740; PIDN:CAA31711.1; PID:g29741

R;Bazil, V.; Baudys, M.; Hilgert, I.; Stefanova, I.; Low, M.G.; Zbrozek, J.; Horejsi, V.

Mol. Immunol. 26, 657-662, 1989

A;Title: Structural relationship between the soluble and membrane-bound forms of human

A;Reference number: PLO108; MUID:89384684; PMID:2779588

A;Accession: PLO108

A;Molecule type: protein

A;Residues: 362-367 <BAZ>

A;Note: the carboxyl-terminal sequence of the soluble CD14 isolated from urine was dete

R;Simmons, D.L.; Tan, S.; Tenen, D.G.; Nicholson-Weller, A.; Seed, B.

Blood 73, 284-289, 1989

A;Title: Monocyte antigen CD14 is a phospholipid anchored membrane protein.

A;Reference number: A30555; MUID:89088540; PMID:2462937

A;Accession: A30555

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-76 'G', 78-186 'C', 188-375 <SIM>

C;Comment: This glycoprotein is expressed primarily on peripheral blood monocytes and m

C;Comment: The protein is anchored to the cell membrane by a phosphatidylinositol linka

C;Genetics:

receptor-like prot
probable LRR recep
tlr protein - frui
ipah protein - Shi
hypothetical prote
hypothetical prote
probable receptor
protein kinase hom
hypothetical prote
hypothetical prote
insulin-like growt
disease resistance
probable serine/th
chondroadherin pre
protein F21B7.6 [i
leucine-rich repea

30 112 6.1 962 2 T04124
31 111.5 6.1 767 2 B84594
32 111.5 6.1 1385 2 T13887
33 111 6.0 574 2 B35149
34 111 6.0 836 2 T46070
35 110.5 6.0 789 2 T52067
36 110.5 6.0 1143 2 B84431
37 110 6.0 1029 2 T00712
38 110 6.0 2756 2 T30183
39 109.5 6.0 679 2 T20713
40 109 5.9 605 2 A41915
41 108.5 5.9 853 2 T17461
42 108.5 5.9 1013 2 T10659
43 107.5 5.8 361 2 A53860
44 107.5 5.8 395 2 A86166
45 107.5 5.8 397 2 T00914

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Wed Oct 6 09:56:25 2004

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001447
; CURRENT APPLICATION NUMBER: US/60/443,566
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 25102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2776
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-60-443-566-2776

Query Match 99.5%; Score 1831; DB 33; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTPEPCELDDERFCVCFSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDERFCVCFSEPOPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRRLKELTLEDLKITGTMPPLPLEA 120
Db 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRRLKELTLEDLKITGTMPPLPLEA 139
QY 121 TGLALSLRLRNVSQWATGRSLAELOQWLKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180
Db 140 TGLALSLRLRNVSQWATGRSLAELOQWLKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 199
QY 181 DLSNPGLGRLMAALCPHKFPAIQNLALRNTGMEPTGVCAALAAAGVQPHSLDLSHN 240
Db 200 DLSNPGLGRLMAALCPHKFPAIQNLALRNTGMEPTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPKGLPAKURVLDLSCNRLNRAFPQDELP 300
Db 260 SLRATVNPSAPRCMWSALNSLNSFAGLEQVPKGLPAKURVLDLSCNRLNRAFPQDELP 319
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Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLLVLLQGARGFA 375

Search completed: October 4, 2004, 17:01:55
Job time : 422 secs

QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGKVLSTIAQHSFAPSVBOVRAFPALTSL 180
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 QY 181 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPTGVCAALAAAGVQPHSLDLSHN 240
 DB 200 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPTGVCAALAAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODDEL 300
 DB 260 SLRATVNSAPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODDEL 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 356
 DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 375

RESULT 13

US-10-331-496A-23
 ; Sequence 23, Application US/10331496A
 ; GENERAL INFORMATION:
 ; APPLICANT: FRANTZ GRETCHEN
 ; APPLICANT: HILLAN, KENNETH J.
 ; APPLICANT: PHILLIPS, HEIDI S.
 ; APPLICANT: POLAKIS, PAUL
 ; APPLICANT: SMITH, VICTORIA
 ; APPLICANT: SPENCER, SUSAN D.
 ; APPLICANT: WILLIAMS, P. MICKEY
 ; APPLICANT: WU, THOMAS D.
 ; APPLICANT: ZHANG, ZEMIN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TITLE OF INVENTION: TREATMENT OF TUMOR
 ; FILE REFERENCE: P5014R1-PCT
 ; CURRENT APPLICATION NUMBER: US/10/331,496A
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 60/345,444
 ; PRIOR FILING DATE: 2002-01-02
 ; PRIOR APPLICATION NUMBER: US 60/351,885
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: US 60/360,065
 ; PRIOR FILING DATE: 2002-02-25
 ; PRIOR APPLICATION NUMBER: US 60/362,004
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/366,869
 ; PRIOR FILING DATE: 2002-03-20
 ; PRIOR APPLICATION NUMBER: US 60/366,284
 ; PRIOR FILING DATE: 2002-03-21
 ; PRIOR APPLICATION NUMBER: US 60/368,679
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: US 60/404,809
 ; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: US 60/405,645
 ; PRIOR FILING DATE: 2002-08-21
 ; NUMBER OF SEQ ID NOS: 95
 ; SEQ ID NO 23
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-331-496A-23

Query Match 99.5%; Score 1831; DB 29; Length 375;
 Best Local Similarity 99.7%; Pred. No. 1.5e-160;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDEDFRCVNFSEFPQDSEAFQCVSAVEIHAAGLNLEPFLKRVDAADP 60
 DB 20 TTPEPCELDDDEDFRCVNFSEFPQDSEAFQCVSAVEIHAAGLNLEPFLKRVDAADP 79
 QY 61 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLELTLEDKITGTWPPLEA 120
 DB 80 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLELTLEDKITGTWPPLEA 139
 QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGKVLSTIAQHSFAPSVBOVRAFPALTSL 180
 DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPGKVLSTIAQHSFAPSVBOVRAFPALTSL 199

DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPGKVLSTIAQHSFAPSVBOVRAFPALTSL 199
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 DB 200 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPTGVCAALAAAGVQPHSLDLSHN 259
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 DB 260 SLRATVNSAPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODDEL 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 356
 DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 375

RESULT 14

US-10-723-860-759
 ; Sequence 759, Application US/10723860
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsburg, Wendy M.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
 ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
 ; FILE REFERENCE: 05882.0193.NPUS01
 ; CURRENT APPLICATION NUMBER: US/10/723,860
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 60/429,739
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 8393
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 759
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-723-860-759

Query Match 99.5%; Score 1831; DB 32; Length 375;
 Best Local Similarity 99.7%; Pred. No. 1.5e-160;
 Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTPEPCELDDDEDFRCVNFSEFPQDSEAFQCVSAVEIHAAGLNLEPFLKRVDAADP 60
 DB 20 TTPEPCELDDDEDFRCVNFSEFPQDSEAFQCVSAVEIHAAGLNLEPFLKRVDAADP 79
 QY 61 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLELTLEDKITGTWPPLEA 120
 DB 80 RQYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSRKLELTLEDKITGTWPPLEA 139
 QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGKVLSTIAQHSFAPSVBOVRAFPALTSL 180
 DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPGKVLSTIAQHSFAPSVBOVRAFPALTSL 199
 QY 181 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPTGVCAALAAAGVQPHSLDLSHN 240
 DB 200 DLSNPGGLGERGLMAALCPHKFPALQNLALRNTGMPETPTGVCAALAAAGVQPHSLDLSHN 259
 QY 241 SLRATVNSAPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODDEL 300
 DB 260 SLRATVNSAPRCMSSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODDEL 319
 QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 356
 DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQARGFA 375

RESULT 15

US-60-443-566-2776
 ; Sequence 2776, Application US/60443566
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: BEGOVICH, Ann

Db 200 DLSNDPGLGERGLMAALCPHKFPALQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 260 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 375

RESULT 10
US-09-791-537-85983
; Sequence 85983, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMEB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85983
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-85983

-Query Match 99.5%; Score 1831; DB 22; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 139
QY 121 TGLALSSRLRNVSMTGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPALTSL 180
Db 140 TGLALSSRLRNVSMTGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPALTSL 199
QY 181 DLSNDPGLGERGLMAALCPHKFPALQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 200 DLSNDPGLGERGLMAALCPHKFPALQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 260 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 375

RESULT 11
US-10-207-655-178
; Sequence 178, Application US/10207655
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 178

; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-178

Query Match 99.5%; Score 1831; DB 28; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 139
QY 121 TGLALSSRLRNVSMTGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPALTSL 180
Db 140 TGLALSSRLRNVSMTGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPALTSL 199
QY 181 DLSNDPGLGERGLMAALCPHKFPALQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 200 DLSNDPGLGERGLMAALCPHKFPALQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 260 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQGARGFA 375

RESULT 12
US-10-219-051B-1203
; Sequence 1203, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 1203
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / CAA29999
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-1203

Query Match 99.5%; Score 1831; DB 28; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 139

; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-31301-3

Query Match 99.5%; Score 1831; DB 1; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 60
DB 20 TTPECELDDEDFRCVCFNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
DB 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
QY 121 TGLALSSRLRLNVSWATGRSMIAELQOQWLKPKGLKVLISIAQAHSFAPFSCQVRAFPALTSL 180
DB 140 TGLALSSRLRLNVSWATGRSMIAELQOQWLKPKGLKVLISIAQAHSFAPFSCQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 240
DB 200 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPOPDDEL 300
DB 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTIVLLQGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTIVLLQGARGFA 375

RESULT 8

PCT-US02-41798A-23
; Sequence 23, Application PC/TUS0241798A
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/41798A
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 23
; LENGTH: 375

; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-41798A-23

Query Match 99.5%; Score 1831; DB 1; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 60
DB 20 TTPECELDDEDFRCVCFNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
DB 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
QY 121 TGLALSSRLRLNVSWATGRSMIAELQOQWLKPKGLKVLISIAQAHSFAPFSCQVRAFPALTSL 180
DB 140 TGLALSSRLRLNVSWATGRSMIAELQOQWLKPKGLKVLISIAQAHSFAPFSCQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 240
DB 200 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPOPDDEL 300
DB 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTIVLLQGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTIVLLQGARGFA 375

RESULT 9

PCT-US03-38193-759
; Sequence 759, Application PC/TUS0338193
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.00PC00
; CURRENT APPLICATION NUMBER: PCT/US03/38193
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 759
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38193-759

Query Match 99.5%; Score 1831; DB 1; Length 375;
Best Local Similarity 99.7%; Pred. No. 1.5e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 60
DB 20 TTPECELDDEDFRCVCFNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 79
QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
DB 80 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
QY 121 TGLALSSRLRLNVSWATGRSMIAELQOQWLKPKGLKVLISIAQAHSFAPFSCQVRAFPALTSL 180
DB 140 TGLALSSRLRLNVSWATGRSMIAELQOQWLKPKGLKVLISIAQAHSFAPFSCQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPATQNLALRNTGMEPTGVCAALAAAGVOPHSLDLSHN 240

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; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-18195

Query Match      100.0%; Score 1840; DB 22; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.2e-161;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPPECELDDEDFRCVCFNFSEFPDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPPECELDDEDFRCVCFNFSEFPDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
Qy 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 139
Qy 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLVLSIAQAHSPAFSVEQVRAFPALTSL 180
Db 140 TGLALSSLRNRVSWATGRSWLAELQWLKPLVLSIAQAHSPAFSVEQVRAFPALTSL 199
Qy 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 240
Db 200 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 259
Qy 241 SLRATVNPSPRCWSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNPSPRCWSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOPDDEL 319
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 375

RESULT 5
US-09-806-158-1
; Sequence 1, Application US/09806158
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shouji et al.
; TITLE OF INVENTION: Method for the measurement of soluble CD14 proteins separately
; FILE REFERENCE: 1110-0284P
; CURRENT APPLICATION NUMBER: US/09/806,158
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-806-158-1

Query Match      99.5%; Score 1831; DB 23; Length 356;
Best Local Similarity 99.7%; Pred. No. 1.4e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTPPECELDDEDFRCVCFNFSEFPDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPPECELDDEDFRCVCFNFSEFPDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Qy 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Qy 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLVLSIAQAHSPAFSVEQVRAFPALTSL 180
Db 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLVLSIAQAHSPAFSVEQVRAFPALTSL 180
Qy 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPRCWSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOPDDEL 300
Db 241 SLRATVNPSPRCWSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOPDDEL 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356

RESULT 6
US-10-240-403-1
; Sequence 1, Application US/10240403
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji et al.
; TITLE OF INVENTION: TLR/CD14 BINDING INHIBITOR
; FILE REFERENCE: 1110-0311P
; CURRENT APPLICATION NUMBER: US/10/240,403
; CURRENT FILING DATE: 2003-05-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-403-1

Query Match      99.5%; Score 1831; DB 28; Length 356;
Best Local Similarity 99.7%; Pred. No. 1.4e-160;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTPPECELDDEDFRCVCFNFSEFPDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPPECELDDEDFRCVCFNFSEFPDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Qy 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Qy 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLVLSIAQAHSPAFSVEQVRAFPALTSL 180
Db 121 TGLALSSLRNRVSWATGRSWLAELQWLKPLVLSIAQAHSPAFSVEQVRAFPALTSL 180
Qy 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTTGVCAALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPRCWSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOPDDEL 300
Db 241 SLRATVNPSPRCWSSALNSLNSFAGLEQVPGKLPKALRVLDLSCNRLNRAPOPDDEL 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356

RESULT 7
PCT-US01-31301-3
; Sequence 3, Application PC/TUS0131301
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Alison E
; APPLICANT: Armstrong, Brock
; APPLICANT: Bentivegna, Steven C
; APPLICANT: Koshy, Beena
; APPLICANT: Parks, Katie E
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE CD14 GENE
; FILE REFERENCE: CD14 MWH-1527PCT
; CURRENT APPLICATION NUMBER: PCT/US01/31301
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,973
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
Db 1 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60

QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120

QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPGIKVLSIAQAHSPAFSYEQVRAFPALTSL 180
Db 121 TGLALSSLRNVSWATGRSWLAELQWLKPGIKVLSIAQAHSPAFSYEQVRAFPALTSL 180

QY 181 DLSNDPGLGERGLMAALCPHKFPALQNLALRNTGMEPTGVCALAAAGVQPHSLDLSHN 240
Db 181 DLSNDPGLGERGLMAALCPHKFPALQNLALRNTGMEPTGVCALAAAGVQPHSLDLSHN 240

QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300

QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGFA 356
Db 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGFA 356

RESULT 2

US-09-721-904A-5
; Sequence 5, Application US/09721904A
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.
; APPLICANT: FILIPP, Dominik
; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
; TITLE OF INVENTION: LAIT/SCD14-PROTEIN
; FILE REFERENCE: 47841/00063
; CURRENT APPLICATION NUMBER: US/09/721, 904A
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: PCT/CA99/00482
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: US 60/086, 884
; PRIOR FILING DATE: 1998-05-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Wordperfect 9.0
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
; ORGANISM: human
US-09-721-904A-5

Query Match 100.0%; Score 1840; DB 21; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.2e-161;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
Db 20 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 79

QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 139

QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPGIKVLSIAQAHSPAFSYEQVRAFPALTSL 180
Db 140 TGLALSSLRNVSWATGRSWLAELQWLKPGIKVLSIAQAHSPAFSYEQVRAFPALTSL 199

QY 181 DLSNDPGLGERGLMAALCPHKFPALQNLALRNTGMEPTGVCALAAAGVQPHSLDLSHN 240
Db 200 DLSNDPGLGERGLMAALCPHKFPALQNLALRNTGMEPTGVCALAAAGVQPHSLDLSHN 259

QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 319

QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGFA 356
Db 320 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGFA 375

RESULT 3

US-09-721-904B-5
; Sequence 5, Application US/09721904B
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.
; APPLICANT: FILIPP, Dominik
; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
; TITLE OF INVENTION: LAIT/SCD14-PROTEIN
; FILE REFERENCE: 47841/00063
; CURRENT APPLICATION NUMBER: US/09/721, 904B
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: PCT/CA99/00482
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: US 60/086, 884
; PRIOR FILING DATE: 1998-05-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Wordperfect 9.0
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
; ORGANISM: human
US-09-721-904B-5

Query Match 100.0%; Score 1840; DB 21; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.2e-161;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 60
Db 20 TTPEPCELDEDFRCVNFSEPODSEAFQCVSAVEVEIHAGGLNLEPFLKRVADADP 79

QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 120
Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPPLPLEA 139

QY 121 TGLALSSLRNVSWATGRSWLAELQWLKPGIKVLSIAQAHSPAFSYEQVRAFPALTSL 180
Db 140 TGLALSSLRNVSWATGRSWLAELQWLKPGIKVLSIAQAHSPAFSYEQVRAFPALTSL 199

QY 181 DLSNDPGLGERGLMAALCPHKFPALQNLALRNTGMEPTGVCALAAAGVQPHSLDLSHN 240
Db 200 DLSNDPGLGERGLMAALCPHKFPALQNLALRNTGMEPTGVCALAAAGVQPHSLDLSHN 259

QY 241 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 260 SLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 319

QY 301 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGFA 356
Db 320 EVDNLTLDGNPLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTLVLLQGARGFA 375

RESULT 4

US-09-791-537-18195
; Sequence 18195, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18195

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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:49:12 ; Search time 418 Seconds
(without alignments)
831.280 Million cell updates/sec

Title: US-09-807-709D-1
Perfect score: 1840
Sequence: 1 TTPPECELDDEDFRCVCFNS.....TLGVGVGTLVLLQARGFA 356

Scoring table: BLOSUM62
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Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main.*
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28: /cgn2_6/ptodata/2/paa/US102 COMB.rep.*
29: /cgn2_6/ptodata/2/paa/US103 COMB.rep.*
30: /cgn2_6/ptodata/2/paa/US104 COMB.rep.*
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32: /cgn2_6/ptodata/2/paa/US107 COMB.rep.*
33: /cgn2_6/ptodata/2/paa/US60 COMB.rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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Best Local Similarity	100.0%	Pred. No. 2.1e-161;			

1	1840	100.0	356	23	US-09-807-709A-1	Sequence 1, Appli
2	1840	100.0	375	21	US-09-721-904A-5	Sequence 5, Appli
3	1840	100.0	375	21	US-09-721-904B-5	Sequence 5, Appli
4	1840	100.0	375	22	US-09-791-537-18195	Sequence 18195, A
5	1831	99.5	356	23	US-09-806-158-1	Sequence 1, Appli
6	1831	99.5	356	28	US-10-240-403-1	Sequence 1, Appli
7	1831	99.5	375	1	PCT-US01-31301-3	Sequence 3, Appli
8	1831	99.5	375	1	PCT-US02-41798A-23	Sequence 23, Appli
9	1831	99.5	375	1	PCT-US03-38193-759	Sequence 759, App
10	1831	99.5	375	22	US-09-791-537-85983	Sequence 85983, A
11	1831	99.5	375	28	US-10-207-655-178	Sequence 1203, Ap
12	1831	99.5	375	28	US-10-219-051B-1203	Sequence 23, Appli
13	1831	99.5	375	29	US-10-331-496A-23	Sequence 759, App
14	1831	99.5	375	32	US-10-723-860-759	Sequence 2776, Ap
15	1831	99.5	375	33	US-60-443-566-2776	Sequence 24579, A
16	1831	99.5	375	33	US-60-452-680-24579	Sequence 15312, A
17	1831	99.5	375	33	US-60-453-050-15312	Sequence 15312, A
18	1831	99.5	375	33	US-60-453-135-15312	Sequence 15312, A
19	1831	99.5	375	33	US-60-455-444-8501	Sequence 8501, Ap
20	1831	99.5	375	33	US-60-465-241-8501	Sequence 8501, Ap
21	1831	99.5	375	33	US-60-466-412-15312	Sequence 15312, A
22	1831	99.5	375	33	US-60-487-610-2787	Sequence 2787, Ap
23	1831	99.5	404	21	US-09-724-676-59178	Sequence 59178, A
24	1831	99.5	404	21	US-09-724-678A-59178	Sequence 59178, A
25	1827	99.3	356	30	US-10-432-236-1	Sequence 1, Appli
26	1827	99.3	375	22	US-09-791-537-47508	Sequence 47508, A
27	1807	98.2	431	1	PCT-US00-05918-485	Sequence 485, App
28	1807	98.2	431	24	US-09-925-302-485	Sequence 45, Appl
29	1791	97.3	348	7	US-08-366-953B-45	Sequence 45, Appl
30	1791	97.3	348	7	US-08-366-953B-45	Sequence 27, Appl
31	1791	97.3	348	8	US-08-484-397-27	Sequence 45, Appl
32	1791	97.3	348	13	US-08-976-944-45	Sequence 27, Appl
33	1764	95.9	348	8	US-08-484-397-3	Sequence 3, Appli
34	1764	95.9	348	8	US-08-484-397-7	Sequence 7, Appli
35	1764	95.9	348	8	US-08-484-397-4	Sequence 4, Appli
36	1763	95.8	348	8	US-08-484-397-5	Sequence 5, Appli
37	1763	95.8	348	8	US-08-484-397-6	Sequence 6, Appli
38	1762	95.8	348	8	US-08-484-397-2	Sequence 2, Appli
39	1710	92.9	334	8	US-08-484-397-8	Sequence 8, Appli
40	1650	89.7	339	18	US-09-443-638B-1	Sequence 1, Appli
41	1633	88.8	339	28	US-10-251-718-1	Sequence 1, Appli
42	1576	85.7	360	22	US-09-758-470-519	Sequence 519, App
43	1576	85.7	360	28	US-10-211-818-519	Sequence 519, App
44	1420	77.2	407	1	PCT-US01-08631-51702	Sequence 51702, A
45	1328.5	72.2	373	21	US-09-721-904A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-807-709A-1
; Sequence 1, Application US/09807709A
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; TITLE OF INVENTION: PROTEIN FOR TREATMENT OR PREVENTION OF G.I. TRACT DISORDER
; FILE REFERENCE: 113308-002
; CURRENT APPLICATION NUMBER: US/09/807,709A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/EP99/07911
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP98203501.6
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-709A-1

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 160326
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_115793C.1.pap
US-10-424-599-160326

Query Match
Best Local Similarity 16.0%; Score 295; DB 12; Length 75;
Matches 52; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPECELDDEDFRCVCFSEFQDWEAFQCVSAVEIHAAGLNLEPFLKRVDA 56
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Db 20 TTPECELDDEDFRCVCFSEFQDWEAFQCVSAVEIHAAGLNLEPFLKRVDA 75

RESULT 14
US-10-240-403-2
; Sequence 2, Application US/10240403
; Publication No. US20040092712A1
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji et al.
; TITLE OF INVENTION: TLR/CD14 BINDING INHIBITOR
; FILE REFERENCE: 1110-0311P
; CURRENT APPLICATION NUMBER: US/10/240,403
; CURRENT FILING DATE: 2003-05-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-403-2

*Query Match
Best Local Similarity 13.4%; Score 247; DB 16; Length 47;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 LEQVPKGLPAKLRVLDLSCNRLNRAPODELPEVDNLTLDGNPFLVP 315
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Db 1 LEQVPKGLPAKLRVLDLSCNRLNRAPODELPEVDNLTLDGNPFLVP 47

RESULT 15
US-10-432-236-2
; Sequence 2, Application US/10432236
; Publication No. US20040091478A1
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji
; APPLICANT: SHIRAKAWA, Kamon
; APPLICANT: MORI, Sadao
; TITLE OF INVENTION: ANTI CD14 MONOCLONAL ANTIBODY HAVING AN EFFECT OF INHIBITING CD14
; FILE REFERENCE: 1110-0315P
; CURRENT APPLICATION NUMBER: US/10/432,236
; CURRENT FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: human
US-10-432-236-2

Query Match
Best Local Similarity 13.4%; Score 247; DB 16; Length 47;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 LEQVPKGLPAKLRVLDLSCNRLNRAPODELPEVDNLTLDGNPFLVP 315
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Db 1 LEQVPKGLPAKLRVLDLSCNRLNRAPODELPEVDNLTLDGNPFLVP 47

Search completed: October 4, 2004, 17:06:09
Job time : 134 secs

Db 198 SDNPELGERGLISALCPLKFTLQVLALRNAGMETPSGVCSSALAAARVQLQGLDLSHNSL 257
Qy 243 RATVNPSPRCWMSALNSLNSFAGLEQVPGKLPKLVLDLSCNRLNRAPOQDELPEV 302
Db 258 RDAA--GAPSCDWPQSLNSLNSFTGLKQVPGKLPKLVLDLSCNRLNRAPOQDELPEV 315
Qy 303 DNLTLGDPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSTLVLQARGF 355
Db 316 GNLSLKGPNFL--DSESHSEKFNKNSGVVVTAGAPSSQAVALSOTLALLGDRLF 365

RESULT 10
US-10-281-478-10
; Sequence 10, Application US/10281478
; Publication No. US20030108959A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Johnson, Richard S.
; APPLICANT: Guo, Lin
; APPLICANT: Mahimkar, Rajeev M.
; APPLICANT: Peschon, Jacques J.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: TREATING DISEASES MEDIATED BY METALLOPROTEASE-SHED PROTEINS
; FILE REFERENCE: 3327-A
; CURRENT APPLICATION NUMBER: US/10/281,478
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-281-478-10

Query Match 61.8%; Score 1136.5; DB 14; Length 366;
Best Local Similarity 65.7%; Pred. No. 5e-101;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;
Qy 3 PEPCELDDEDFRCVNFSEPODWSFAFCVSAVEIHAAGLNLEPFLKRVADADPRQ 62
Db 20 PEPCELDEES--CSCNFDKPKDMSAFNCIGAADVELYGGRSLEYLLKRVDEADLQ 77
Qy 63 YADTVKALRVRLTVGAQVPAQLVGLALRVLAYSRKELTLEDLKITGTPPLLEATG 122
Db 78 FTDIKSLKRLTVRAARIPSRILFGALRVIGISGLQELTLENLEVTGTAPPLLEATG 137
Qy 123 LALSRLRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSEYQVRAFPALTSIDL 182
Db 138 PDNLNLRNVSATGRSWLAELQWLKPKLVLSIAQAHSLNFSCEQVRVFPALSTLDL 197
Qy 183 SDNPELGERGLISALCPLKFTLQVLALRNAGMETPSGVCSSALAAARVQLQGLDLSHNSL 242
Db 198 SDNPELGERGLISALCPLKFTLQVLALRNAGMETPSGVCSSALAAARVQLQGLDLSHNSL 257
Qy 243 RATVNPSPRCWMSALNSLNSFAGLEQVPGKLPKLVLDLSCNRLNRAPOQDELPEV 302
Db 258 RDAA--GAPSCDWPQSLNSLNSFTGLKQVPGKLPKLVLDLSCNRLNRAPOQDELPEV 315
Qy 303 DNLTLGDPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSTLVLQARGF 355
Db 316 GNLSLKGPNFL--DSESHSEKFNKNSGVVVTAGAPSSQAVALSOTLALLGDRLF 365

RESULT 11
US-10-029-386-30234
; Sequence 30234, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/029,386

; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30234
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHES.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P08571, EVALUATE 2.00e-48
US-10-029-386-30234

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Best Local Similarity 98.9%; Pred. No. 3.3e-38;
Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 131 RNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSEYQVRAFPALTSIDLSDNPGIGE 190
Db 1 RNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSEYQVRAFPALTSIDLSDNPGIGE 60
Qy 191 RGLMAALCPHKFPFAIQNLALRNTGMTPTGVC 222
Db 61 RGLMAALCPHKFPFAIQNLALRNTGMTPTGVC 92

RESULT 12
US-10-131-433-7
; Sequence 7, Application US/10131433
; Publication No. US20030054422A1
; GENERAL INFORMATION:
; APPLICANT: UNILEVER, PLC
; TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
; FILE REFERENCE: Lipopolysaccharide Immunoassay
; CURRENT APPLICATION NUMBER: US/10/131,433
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US/09/545,180
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Lapine
US-10-131-433-7

Query Match 16.9%; Score 310.5; DB 14; Length 59;
Best Local Similarity 96.7%; Pred. No. 2.8e-22;
Matches 58; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Db 1 TTPPECELDDEDFRCVNFSEPODWSFAFCVSAVEIHAAGLNLEPFLKRV-ADADPR 59

RESULT 13
US-10-424-599-160326
; Sequence 160326, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

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Db 337 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGAR 389
RESULT 7
US-10-251-718-1
; Sequence 1, Application US/10251718
; Publication No. US20030114377A1
; GENERAL INFORMATION:
; APPLICANT: Kirikland, Theo N.
; APPLICANT: Viriyakosol, Suganya
; TITLE OF INVENTION: Inhibition therapy for septic shock with mutant CD14
; FILE REFERENCE: 6627-PA8068
; CURRENT APPLICATION NUMBER: US/10/251,718
; PRIOR FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2002-11-26
; PRIOR FILING DATE: 09/433,638
; PRIOR FILING DATE: 1999-11-18
; PRIOR FILING DATE: 60/109227
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (326)..(339)
; OTHER INFORMATION: residues are contributed by linker and vector
US-10-251-718-1
Query Match 88.8%; Score 1633; DB 14; Length 339;
Best Local Similarity 97.3%; Pred. No. 4.2e-149;
Matches 319; Conservative 1; Mismatches 6; Indels 2; Gaps 2;
QY 1 TTEPCELDDEDFRCVCFNFPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTEPCELDDEDFRCVCFNFPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPLEATG 120
Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPLEATG 120
QY 121 TGLSSLRRLNVSWATGRSWLAELQWLKPKLVLSIAQAHSFAPSYEQVRAFPALTS 180
Db 121 TGLSSLRRLNVSWATGRSWLAELQWLKPKLVLSIAQAHSFAPSYEQVRAFPALTS 180
QY 181 DLSNPGLGERGLMAALCPHK-FAIONLAL-RNTGNETPTGVCALAAAGVQPHSLDLS 238
Db 181 DLSNPGLGERGLMAALCPHKFPFAIONLALPRNTGNETPTGVCALAAAGVQPHSLDLS 240
QY 239 HNSLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODE 298
Db 241 HNSLRATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODE 300
QY 299 LPEVDNLTLDGNPFLVPGTALPHEGSMN 326
Db 301 LPEVDNLTLDGNPFLVPGTALPHEGERP 328
RESULT 8
US-09-870-759-72
; Sequence 72, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE: 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 72
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-72
Query Match 61.8%; Score 1136.5; DB 10; Length 366;
Best Local Similarity 65.7%; Pred. No. 5e-101;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;
QY 3 PEPCEDDEDFRCVCFNFPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 62
Db 20 PEPCEDDEES--CSCNFPDQWSEAFNCLGAADVLYGGGRSLEYLLKRVDTADLQ 77
QY 63 YADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPLEATG 122
Db 78 FTDIISLSLKELTVRAARIPSRILFGALRVLSIGLQELTLENLEVTGTAPPPLLEATG 137
QY 123 LALSSLRRLNVSWATGRSWLAELQWLKPKLVLSIAQAHSFAPSYEQVRAFPALTS 182
Db 138 PDNLINLRNVSWATRDAMLAELOQWLKPKLVLSIAQAHSNLFSCFQVRAFPALSTLD 197
QY 183 SDNPGI GERGLMAALCPHKFAIONLALRNTGNETPTGVCALAAAGVQPHSLDLS 242
Db 198 SDNPGI GERGLISALCPKFPFTQLVLRNAGMETPGVCSALAAARVOLQGLDLSHNSL 257
QY 243 RATVNSAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODEP 302
Db 258 RDA--GAPSCDWPQSLNSLNSFTGLKQVPGKLPKLVLDLSCNRLNRAPODEP 315
QY 303 DNLITLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGAR 355
Db 316 GNLSLKGPNFL--DSSEHSEKFNKSVVTVAGAPSSQVALSGTLLALLGDLRF 365
RESULT 9
US-09-751-708A-72
; Sequence 72, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; PRIOR FILING DATE: 2002-10-15
; PRIOR FILING DATE: 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 72
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-751-708A-72
Query Match 61.8%; Score 1136.5; DB 10; Length 366;
Best Local Similarity 65.7%; Pred. No. 5e-101;
Matches 232; Conservative 40; Mismatches 74; Indels 7; Gaps 3;
QY 3 PEPCEDDEDFRCVCFNFPDQWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 62
Db 20 PEPCEDDEES--CSCNFPDQWSEAFNCLGAADVLYGGGRSLEYLLKRVDTADLQ 77
QY 63 YADTVKALVRRLTVGAQVPAQLLVGALRVLAISRLKELTLEDKLTGTMPLEATG 122
Db 78 FTDIISLSLKELTVRAARIPSRILFGALRVLSIGLQELTLENLEVTGTAPPPLLEATG 137
QY 123 LALSSLRRLNVSWATGRSWLAELQWLKPKLVLSIAQAHSFAPSYEQVRAFPALTS 182
Db 138 PDNLINLRNVSWATRDAMLAELOQWLKPKLVLSIAQAHSNLFSCFQVRAFPALSTLD 197
QY 183 SDNPGI GERGLMAALCPHKFAIONLALRNTGNETPTGVCALAAAGVQPHSLDLS 242
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; TYPE: PRT
; ORGANISM: human
US-10-432-236-1

Query Match      99.3%; Score 1827; DB 16; Length 356;
Best Local Similarity 99.4%; Pred. No. 7.8e-168;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 TTPEPCELDDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60

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Db 61 ROYADTVKALRVRLTVGAQAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLPLEA 120

QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFAFSYEQVRAFPALTSL 180
Db 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFAFSYEQVRAFPALTSL 180

QY 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240

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Db 241 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARGFA 356

RESULT 5
US-09-925-302-485
; Sequence 485, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 485
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (263)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (264)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-485

Query Match      98.2%; Score 1807; DB 9; Length 431;
Best Local Similarity 99.2%; Pred. No. 8.8e-166;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTPEPCELDDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 37 TTPEPCELDDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 96

QY 61 ROYADTVKALRVRLTVGAQAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLPLEA 120
Db 97 ROYADTVKALRVRLTVGAQAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLPLEA 156

QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFAFSYEQVRAFPALTSL 180
Db 157 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFAFSYEQVRAFPALTSL 216

QY 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 217 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 276

QY 241 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 277 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 336

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARG 353
Db 337 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARG 389

RESULT 6
US-09-925-302-485
; Sequence 485, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 485
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (263)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (264)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-485

Query Match      98.2%; Score 1807; DB 12; Length 431;
Best Local Similarity 99.2%; Pred. No. 8.8e-166;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 37 TTPEPCELDDDEDFRCVCFSEFQPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 96

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QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFAFSYEQVRAFPALTSL 180
Db 157 TGLALSSRLRNVSATGRSWLAELQWLKPGIKVLSIAQAHSFAFSYEQVRAFPALTSL 216

QY 181 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
Db 217 DLSNDFGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 276

QY 241 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 300
Db 277 SLRATVNPSPAPRCMWSALNSLNSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDDEL 336

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARG 353
Db 337 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQGARG 389
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:54:27 ; Search time 131 Seconds

(without alignments)
874.508 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

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Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

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Database : Published Applications AA:*

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1831	99.5	356	16 US-10-240-403-1	Sequence 1, Appli
2	1831	99.5	375	14 US-10-207-655-178	Sequence 178, App
3	1831	99.5	375	15 US-10-331-496A-23	Sequence 23, Appl
4	1827	99.3	356	16 US-10-432-236-1	Sequence 1, Appli
5	1807	98.2	431	9 US-09-325-302-485	Sequence 485, App
6	1807	98.2	431	12 US-09-925-302-485	Sequence 485, App
7	1633	88.8	339	14 US-10-251-718-1	Sequence 1, Appli
8	1136.5	61.8	366	9 US-09-870-759-72	Sequence 72, Appl
9	1136.5	61.8	366	10 US-09-751-708A-72	Sequence 10, Appl
10	1136.5	61.8	366	14 US-10-281-478-10	Sequence 30234, A
11	478	26.0	92	14 US-10-029-386-30234	Sequence 7, Appli
12	310.5	16.9	59	14 US-10-131-433-7	Sequence 160326,
13	295	16.0	75	12 US-10-424-599-160326	Sequence 2, Appli
14	247	13.4	47	16 US-10-240-403-2	Sequence 2, Appli
15	247	13.4	47	16 US-10-432-236-2	Sequence 2, Appli

16	152	8.3	971	16	US-10-437-963-116887	Sequence 116887,
17	150	8.2	1128	16	US-10-437-963-179464	Sequence 179464,
18	148.5	8.1	733	16	US-10-437-963-200675	Sequence 200675,
19	148	8.0	702	12	US-10-425-114-45322	Sequence 45322, A
20	147.5	8.0	784	10	US-09-950-041-4	Sequence 4, Appli
21	147.5	8.0	784	12	US-10-456-947-46	Sequence 46, Appli
22	147.5	8.0	784	13	US-10-145-014-23	Sequence 23, Appl
23	147.5	8.0	784	14	US-10-095-627-12	Sequence 12, Appl
24	147.5	8.0	784	16	US-10-732-563-4	Sequence 4, Appli
25	144.5	7.9	353	10	US-09-759-1308-193	Sequence 193, App
26	144.5	7.9	353	10	US-09-946-374-397	Sequence 397, App
27	144.5	7.9	353	11	US-09-833-245-99	Sequence 99, Appl
28	144.5	7.9	353	11	US-09-833-245-100	Sequence 100, App
29	144.5	7.9	353	12	US-10-006-485A-397	Sequence 397, App
30	144.5	7.9	353	12	US-10-013-907A-397	Sequence 397, App
31	144.5	7.9	353	12	US-10-015-499A-397	Sequence 397, App
32	144.5	7.9	353	12	US-10-013-910A-397	Sequence 397, App
33	144.5	7.9	353	12	US-10-226-254A-397	Sequence 397, App
34	144.5	7.9	353	12	US-10-015-395A-397	Sequence 397, App
35	144.5	7.9	353	14	US-10-006-856A-397	Sequence 397, App
36	144.5	7.9	353	14	US-10-006-818A-397	Sequence 397, App
37	144.5	7.9	353	14	US-10-015-393A-397	Sequence 397, App
38	144.5	7.9	353	14	US-10-015-869A-397	Sequence 397, App
39	144.5	7.9	353	14	US-10-012-121A-397	Sequence 397, App
40	144.5	7.9	353	14	US-10-006-116A-397	Sequence 397, App
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42	144.5	7.9	353	14	US-10-017-527A-397	Sequence 397, App
43	144.5	7.9	353	14	US-10-013-913A-397	Sequence 397, App
44	144.5	7.9	353	14	US-10-007-194A-397	Sequence 397, App
45	144.5	7.9	353	14	US-10-013-430A-397	Sequence 397, App

ALIGNMENTS

RESULT 1
US-10-240-403-1
; Sequence 1, Application US/10240403
; Publication NO. US20040092712A1
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji et al.
; TITLE OF INVENTION: TLR/CD14 BINDING INHIBITOR
; FILE REFERENCE: 1110-0311P
; CURRENT APPLICATION NUMBER: US/10/240,403
; CURRENT FILING DATE: 2003-05-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-403-1

Query Match 99.5%; Score 1831; DB 16; Length 356;
Best Local Similarity 99.7%; Pred. No. 3.2e-168;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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us-09-807-709d-1.rai

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RESULT 14

US-08-746-883-4
 ; Sequence 4, Application US/08746883
 ; Patent No. 603693
 ; GENERAL INFORMATION:
 ; APPLICANT: Julius, Michael H., Filipp, Dominic,
 ; APPLICANT: Alizadeh-Khavi, Kamel
 ; TITLE OF INVENTION: B Cell Activation
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; COUNTRY: Canada
 ; ZIP: M5L 1A9
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/746,883
 ; FILING DATE: No. 6093693ember 18, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 47841/00008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 373 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-746-883-4

Query Match 72.2%; Score 1328.5; DB 3; Length 373;
 Best Local Similarity 74.2%; Pred. No. 1.6e-130;
 Matches 264; Conservative 32; Mismatches 55; Indels 5; Gaps 4;
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 Db 22 TTEPCELDDEDFRCVCFNFTDPKPDSSAVQCMVAVEISAGRSLEQFLK--GADTNPK 79
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 Db 80 QYADTIKALRVRLKLGAAQVPAQLLVAVLRALGYSRLKELTLEDLEVTGPTTPLEAA 139
 QY 122 GLALSSRLRNVSATGRSWLAELQOWLKPLKVLSTIAQAHSPAFSYEQVRAFALTSLD 181
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 QY 182 LSNPGLGERGLMAALCPHKFPALQNLALRNTGMETPTGVCALAAAGVOPHSLDLSHNS 241
 Db 200 LSDNPSLGTGLMAALCPNKFPAQYALALRNAGMETPFGVCAALAAARVQPSLDLSHNS 259
 QY 242 LRATVNPSPRCWMSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOQDELPE 301
 Db 260 LRVTA-PGATRCVMPALRSNLNSFAGLEQVPKGLPPKLSVLDLSCNKLRSRPRDELPE 318
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 Db 319 VNDLTLDGNPFVDPG-ALQHQNDPMISGVVPACARSALTMTGVSALALLQARGFA 373

RESULT 15

US-09-313-177-4
 ; Sequence 4, Application US/09313177
 ; Patent No. 6676985

; GENERAL INFORMATION:
 ; APPLICANT: JULIUS, Michael H.; FILIPP, Dominik;
 ; APPLICANT: ALIZADEH-KHIAVI, Kamel
 ; TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
 ; TITLE OF INVENTION: PROTEIN (CD14), ENCODING GENE AND APPLICATION
 ; TITLE OF INVENTION: IN B CELL ACTIVATION
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5L 1A9
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/313,177
 ; FILING DATE: May 18, 1999
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/746,883
 ; FILING DATE: No. 6676985ember 18, 1996
 ; APPLICATION NUMBER: PCT/CA 97/00880
 ; FILING DATE: No. 6676985ember 18, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 47841/00047
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 373 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-313-177-4

Query Match 72.2%; Score 1328.5; DB 4; Length 373;
 Best Local Similarity 74.2%; Pred. No. 1.6e-130;
 Matches 264; Conservative 32; Mismatches 55; Indels 5; Gaps 4;
 QY 2 TPEPCELDDEDFRCVCFSEPPQDWSAEFCVSAVEIHAGGLNLPFLKRVVDADPR 61
 Db 22 TTEPCELDDEDFRCVCFNFTDPKPDSSAVQCMVAVEISAGRSLEQFLK--GADTNPK 79
 QY 62 QYADTVKALRVRLTVGAAGVPAQLLVGALRVLAYSKELTLEDLKITGMPPLPLEAT 121
 Db 80 QYADTIKALRVRLKLGAAQVPAQLLVAVLRALGYSRLKELTLEDLEVTGPTTPLEAA 139
 QY 122 GLALSSRLRNVSATGRSWLAELQOWLKPLKVLSTIAQAHSPAFSYEQVRAFALTSLD 181
 Db 140 GPALTILSLRNVSMTTGGAWLGELQOWLKPLKVLSTIAQAHSLAFPCAGLSTFEALTLLD 199
 QY 182 LSNPGLGERGLMAALCPHKFPALQNLALRNTGMETPTGVCALAAAGVOPHSLDLSHNS 241
 Db 200 LSDNPSLGTGLMAALCPNKFPAQYALALRNAGMETPFGVCAALAAARVQPSLDLSHNS 259
 QY 242 LRATVNPSPRCWMSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOQDELPE 301
 Db 260 LRVTA-PGATRCVMPALRSNLNSFAGLEQVPKGLPPKLSVLDLSCNKLRSRPRDELPE 318
 QY 302 VDNLTLDGNPFVPGTALPHEGS-MNSGVVPACARSTLSVGSVGTLLVLIQARGFA 356
 Db 319 VNDLTLDGNPFVDPG-ALQHQNDPMISGVVPACARSALTMTGVSALALLQARGFA 373

Search completed: October 4, 2004, 17:02:32

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 12
US-08-484-397A-2
; Sequence 2, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-397A-2

Query Match 95.8%; Score 1762; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 6e-176; Indels 0; Gaps 0;
Matches 343; Conservative 0; Mismatches 5;

QY 1 TTPEFCBLDDDFRCVCFNFPDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 60
Db 1 TTPEFCGGGDDDFRCVCFNFPDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADP 60

QY 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
Db 61 ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120

QY 121 TGLALSSLRUNVSWATGRSLAELOQWLKPLKVLSTAQAHSPAFSVEQVRAPFALTSL 180
Db 121 TGLALSSLRUNVSWATGRSLAELOQWLKPLKVLSTAQAHSPAFSVEQVRAPFALTSL 180

QY 181 DLSNPGGLGERGLMAALCPHFPAITQNLALRNTGNETPTGVCALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGGLGERGLMAALCPHFPAITQNLALRNTGNETPTGVCALAAAGVQPHSLDLSHN 240

QY 241 SLRATVNPSPAPCMWSSALNSLNSFAGLEQVPGKLPKALRVLDLSNRLNRPAPQDEL 300
Db 241 SLRATVNPSPAPCMWSSALNSLNSFAGLEQVPGKLPKALRVLDLSNRLNRPAPQDEL 300

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 13
US-08-484-397A-8
; Sequence 8, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-397A-8

Query Match 92.9%; Score 1710; DB 2; Length 334;
Best Local Similarity 99.7%; Pred. No. 1.6e-170; Indels 0; Gaps 0;
Matches 333; Conservative 0; Mismatches 1;

QY 15 CVCNFPDQDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADPRQYADTVKALRVRR 74
Db 1 CVCNFPDQDWEAFQCVSAVEVEIHAGGLNLEPFLKRVDDADADPRQYADTVKALRVRR 60

QY 75 LTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEATGLALSSLRNVS 134
Db 61 LTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEATGLALSSLRNVS 120

QY 135 WATGRSLAELOQWLKPLKVLSTAQAHSPAFSVEQVRAPFALTSLDSDNPGGLGERGLM 194
Db 121 WATGRSLAELOQWLKPLKVLSTAQAHSPAFSVEQVRAPFALTSLDSDNPGGLGERGLM 180

QY 195 AALCPHFPAITQNLALRNTGNETPTGVCALAAAGVQPHSLDLSHNSLEATVNPSPAPCM 254
Db 191 AALCPHFPAITQNLALRNTGNETPTGVCALAAAGVQPHSLDLSHNSLEATVNPSPAPCM 240

QY 255 WSSALNSLNSFAGLEQVPGKLPKALRVLDLSNRLNRPAPQDELPEVDNLTLDGNPFLV 314
Db 241 WSSALNSLNSFAGLEQVPGKLPKALRVLDLSNRLNRPAPQDELPEVDNLTLDGNPFLV 300

QY 315 PGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
Db 301 PGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

QY 241 SURATVNSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
DB 241 SURATVNSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 10

US-08-484-397A-5
; Sequence 5, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-5

Query Match 95.8%; Score 1763; DB 2; Length 348;
Best Local Similarity 98.9%; Pred. No. 4.7e-176;
Matches 344; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTPEPCBLDEDFRCVCFNFPQDWEAFQCVSAVEVEIHAGLNLEPFLKRVADADP 60
DB 1 TTPEPCBLLEDFRCVCFNFPQDWEAFQCVSAVEVEIHAGLNLEPFLKRVADADP 60
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPLPLEA 120
DB 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPLPLEA 120
QY 121 TGLALSLRLNVSWSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
DB 121 TGLALSLRLNVSWSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
QY 181 DLSNDPGLGERGLMAALCPHKFPFQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPLPLEA 240
DB 181 DLSNDPGLGERGLMAALCPHKFPFQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPLPLEA 240
QY 241 SURATVNSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300

DB 241 SURATVNSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 11

US-08-484-397A-6
; Sequence 6, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-6

Query Match 95.8%; Score 1763; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 4.7e-176;
Matches 343; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTPEPCBLDEDFRCVCFNFPQDWEAFQCVSAVEVEIHAGLNLEPFLKRVADADP 60
DB 1 TTPEPCBLLEDFRCVCFNFPQDWEAFQCVSAVEVEIHAGLNLEPFLKRVADADP 60
QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPLPLEA 120
DB 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPLPLEA 120
QY 121 TGLALSLRLNVSWSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
DB 121 TGLALSLRLNVSWSWATGRSWLAELQWLKPKLVLSIAQAHSPAFSCEQVRAFPALTSL 180
QY 181 DLSNDPGLGERGLMAALCPHKFPFQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPLPLEA 240
DB 181 DLSNDPGLGERGLMAALCPHKFPFQVPAQLLVGALRVLAYSLRKELTLEDIKITGTMPPLPLEA 240
QY 241 SURATVNSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300
DB 241 SURATVNSAPRCWSSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPODELP 300

Qy	181	DLSDNPGLGERGLMAALCPHFKEPAIQNALRNTGMETPTGVCAALAAAGVQPHSLDLSLN	240
Db	181	DLSDNPGLGERGLMAALCPHFKEPAIQNALRNTGMETPTGVCAALAAAGVQPHSLDLSLN	240
Qy	241	SLRATVNPSPAPRCMWSNALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPODEL	300
Db	241	SLRATVNPSPAPRCMWSNALNSLNSFAGLEQVPKGLPAKLRLVLDLSCNRLNRAPODEL	300
Qy	301	EVDNMLTDGNPFVLPGTALPHFGSMNSGVVPACARSTLSVGVSGTLVL	348
Db	301	EVDNMLTDGNPFVLPGTALPHFGSMNSGVVPACARSTLSVGVSGTLVL	348

RESULT 8
US-08-484-397A-7
; Sequence 7, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:

	Query Match	95.9%;	Score 1764;	DB 2;	Length 348;
	Best Local Similarity	98.6%;	Prod. No. 3.7e-176;		
	Matches 343;	Conservative	0; Mismatches 15;	Indels 0;	Gaps 0;
Qy	1	TTPEPCELDDEPRFCVNFSEPPQDWSAFCQCSAVEVEIHAGGLNLEPFLKRVADADADP	60		
Db	1	TTPEPCFPPEPRFCVNFSEPPQDWSAFCQCSAVEVEIHAGGLNLEPFLKRVADADADP	60		
Qy	61	QYADVTKALRVRRLLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPEA	120		
Db	61	QYADVTKALRVRRLLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPEA	120		
Qy	121	TGALSSLLRNYSWATGRSWLAELQWLKPGLVLSIAQAHSFAPFSQEVRAPFALATSL	180		
Db	121	TGALSSLLRNYSWATGRSWLAELQWLKPGLVLSIAQAHSFAPFSQEVRAPFALATSL	180		
Qy	181	DISDNPGLGERGHMAALCPHKFPFPAIQNALRNNTGMEPTTGVCAALAAAGVQPHSLDLGHN	240		

181	DLSDNPGLGERGKLMALCPHKFPFAIQNLALANTGMETPTGCAALAAAGVGFPHSLDLSHN	244
Db		
241	SLRATVNPSPRCWSSNALNSLNLSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOQDEL	300
Qy		
241	SLRATVNPSPRCWSSNALNSLNLSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOQDEL	300
Db		
301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVWPCARSTLSVGSGTLVL	348
Qy		
301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVWPCARSTLSVGSGTLVL	348
Dp		

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RESULT 9
US-08-484-397A-4
; Sequence 4, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-484-397A-4

```

	Query Match	95.8%	Score 1763	DB 2	Length 348
	Best Local Similarity	98.6%	Pred. No. 4.7e-176		
	Matches 343	Conservative 1	Mismatches 0	Indels 0	Gaps 0
Qy	1	TTPEPCELDDEDFRCVCFNFSEFPQDWSFAFCVCSAVEVEIHAGINLEPFLKRVDAADP	60		
Db	1	TTPEFCVVVEDFRCVCFNFSEFPQDWSFAFCVCSAVEVEIHAGINLEPFLKRVDAADP	60		
Qy	61	ROYADTVKALRVRRITVGAQAVPAQLLGVALRVLAYSRLKELTLEDLKITGTMPLEP	120		
Db	61	ROYADTVKALRVRRITVGAQAVPAQLLGVALRVLAYSRLKELTLEDLKITGTMPLEP	120		
Qy	121	TGLAUSLLRLNVSWATGRSWLAELQWMLKPLGVLSIAQAHSFAPSVEQVRAPPAITSL	180		
Db	121	TGLAUSLLRLNVSWATGRSWLAELQWMLKPLGVLSIAQAHSFAPSVEQVRAPPAITSL	180		
Qy	181	DUSDNPGLGERGIMAAALCPHKFPATONALRNTGMTPTGVCALAAAGVQPHSLDLSHN	240		
Db	181	DUSDNPGLGERGIMAAALCPHKFPATONALRNTGMTPTGVCALAAAGVQPHSLDLSHN	240		

Db 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALRNTGNETPTGVCAALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPRCWMSALNSLNSFAGLEQVPKGLPAKLRVLDLSNRLNRAPOPDLP 300
Db 241 SLRATVNPSPRCWMSALNSLNSFAGLEQVPKGLPAKLRVLDLSNRLNRAPOPDLP 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 6
US-08-484-397A-38
; Sequence 38 Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7..10
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /label= Xaa
; OTHER INFORMATION: /note= "Xaa is independently selected from Gly, Ala, Val, Leu
; OTHER INFORMATION: Ile and Pro"

US-08-484-397A-38
Query Match 96.0%; Score 1766; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 2.3e-176;
Matches 343; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTPECELDDEDFRCVNFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPEFCXXXEDFRCVNFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Qy 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKITGTMPPLPLEA 120
Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKITGTMPPLPLEA 120
Qy 121 TGLALSSLRNRVNSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180

Db 121 TGLALSSLRNRVNSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180
Qy 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALRNTGNETPTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGGLGERGLMAALCPHKFPAIQNLALRNTGNETPTGVCAALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPRCWMSALNSLNSFAGLEQVPKGLPAKLRVLDLSNRLNRAPOPDLP 300
Db 241 SLRATVNPSPRCWMSALNSLNSFAGLEQVPKGLPAKLRVLDLSNRLNRAPOPDLP 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVL 348

RESULT 7
US-08-484-397A-3
; Sequence 3, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-397A-3

Query Match 95.9%; Score 1764; DB 2; Length 348;
Best Local Similarity 98.6%; Pred. No. 3.7e-176;
Matches 343; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSLKELTLEDKITGTMPPLPLEA 120
Qy 121 TGLALSSLRNRVNSWATGRSWLAELQWLKPKGLKVLSTIAQAHSPAFSVEQVRAFPALTSL 180
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Db 80 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 139
QY 121 TGLALSSLRNRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPPAITSL 180
Db 140 TGLALSSLRNRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPPAITSL 199
QY 181 DLSNPGGLGRGLMAALCPHKFPAIONLARNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
Db 200 DLSNPGGLGRGLMAALCPHKFPAIONLARNTGMEPTTGVCAALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 260 SLRATVNPSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLLQARGFA 375

RESULT 4

US-08-366-953A-45
; Sequence 45, Application US/08366953A
; Patent No. 5766593
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 PEPTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1720
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,953A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook Ph.D., Robert R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-324
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-366-953A-45

Query Match 97.3%; Score 1791; DB 1; Length 348;
Best Local Similarity 99.7%; Pred. No. 5.5e-179;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 120
Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 120
QY 121 TGLALSSLRNRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPPAITSL 180
Db 121 TGLALSSLRNRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPPAITSL 180

QY 181 DLSNPGGLGRGLMAALCPHKFPAIONLARNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGGLGRGLMAALCPHKFPAIONLARNTGMEPTTGVCAALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNPSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
Db 241 SLRATVNPSAPRCWSSALNSLNSFAGLEQVPGKLPKLRVLDLSNRLNRAPOPDDEL 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLL 348
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLTVLL 348

RESULT 5

US-08-484-397A-27
; Sequence 27, Application US/08484397A
; Patent No. 5869055
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-397A-27

Query Match 97.3%; Score 1791; DB 2; Length 348;
Best Local Similarity 99.7%; Pred. No. 5.5e-179;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTPEPCELDDEDFRCVNFSEFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPEPCELDDEDFRCVNFSEFPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
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Db 61 ROYADTVKALVRRLTVGAQVPAQLLVGALRVLAYSRKLTLEDLKITGTMPPLEA 120
QY 121 TGLALSSLRNRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPPAITSL 180
Db 121 TGLALSSLRNRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAPPAITSL 180
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QY 181 DLSNPGGLGERGLMAALCPHKFPAIONLALRNTGMEPTGVCALAAGVQPHSLDLSHN 240
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Db 260 SLRATVNPSAPRCMWSALNSLNSPAGLEQVPGKLPKLRVLDLSNRLNRAPOQDELP 319
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QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQAGGFA 356
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Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQAGGFA 375
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RESULT 2
US-09-313-177-5
; Sequence 5, Application US/09313177
; Patent No. 6676985
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.; Filipp, Dominik;
; APPLICANT: ALIZADEH-KHIAVI, Kameh
; TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
; TITLE OF INVENTION: PROTEIN (CD14), ENCODING GENE AND APPLICATION
; TITLE OF INVENTION: IN B CELL ACTIVATION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/313,177
; FILING DATE: May 18, 1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/746,883
; FILING DATE: No. 6676985ember 18, 1996
; APPLICATION NUMBER: PCT/CA 97/00880
; FILING DATE: No. 6676985ember 18, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 47841/00047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-313-177-5
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Best Local Similarity 100.0%; Pred. No. 4.6e-184;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 80 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
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Db 140 TGLALSLRLNVSWATGRSWLAELQWLKPKGLKVLISIAQHSAPFSEYQVRAFPALTSL 199
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Db 200 DLSNPGGLGERGLMAALCPHKFPAIONLALRNTGMEPTGVCALAAGVQPHSLDLSHN 259
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Db 260 SLRATVNPSAPRCMWSALNSLNSPAGLEQVPGKLPKLRVLDLSNRLNRAPOQDELP 319
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Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSGLVLLQAGGFA 375
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RESULT 3
US-08-205-719-2
; Sequence 2, Application US/08205719
; Patent No. 5705398
; GENERAL INFORMATION:
; APPLICANT: Mintz, D. N.
; APPLICANT: Tobias, P. S.
; APPLICANT: Ulevitch, R. J.
; TITLE OF INVENTION: SYSTEM AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: THERAPEUTIC INHIBITORS OF LPS-MEDIATED SEPSIS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5705398th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,719
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1201P; TSRI324.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-205-719-2
Query Match 99.2%; Score 1826; DB 1; Length 375;
Best Local Similarity 99.4%; Pred. No. 1.3e-182;
Matches 354; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 20 TTPEPCELDDDFRCVNFSEFPQDWSFAFCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
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QY 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
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|

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:51:31 ; Search time 32 Seconds
(without alignments)
574.339 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTPEPCELDEDFRCVNFNS.....TLGVGVGTLVLLQGARGFA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*

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5: /cgn2_6/prodata/2/iaa/PCRU COMB.pep.*

6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1840	100.0	375	US-08-746-883-5	Sequence 5, Appli
2	1840	100.0	375	US-09-313-177-5	Sequence 5, Appli
3	1826	99.2	375	US-08-205-719-2	Sequence 2, Appli
4	1791	97.3	348	US-08-366-953A-45	Sequence 45, Appli
5	1791	97.3	348	US-08-484-397A-27	Sequence 27, Appli
6	1766	96.0	348	US-08-484-397A-38	Sequence 38, Appli
7	1764	95.9	348	US-08-484-397A-3	Sequence 3, Appli
8	1764	95.9	348	US-08-484-397A-7	Sequence 7, Appli
9	1763	95.8	348	US-08-484-397A-4	Sequence 4, Appli
10	1763	95.8	348	US-08-484-397A-5	Sequence 5, Appli
11	1763	95.8	348	US-08-484-397A-6	Sequence 6, Appli
12	1762	95.8	348	US-08-484-397A-2	Sequence 2, Appli
13	1710	92.9	334	US-08-484-397A-8	Sequence 8, Appli
14	1328.5	72.2	373	US-08-746-883-4	Sequence 4, Appli
15	1328.5	72.2	373	US-09-313-177-4	Sequence 4, Appli
16	1136.5	61.8	366	US-08-746-883-6	Sequence 6, Appli
17	1136.5	61.8	366	US-09-313-177-6	Sequence 6, Appli
18	765	41.6	152	US-08-484-397A-10	Sequence 10, Appli
19	765	41.6	152	US-08-484-397A-14	Sequence 14, Appli
20	764	41.5	152	US-08-484-397A-11	Sequence 11, Appli
21	764	41.5	152	US-08-484-397A-12	Sequence 12, Appli
22	764	41.5	152	US-08-484-397A-13	Sequence 13, Appli
23	763	41.5	152	US-08-484-397A-9	Sequence 9, Appli
24	711	38.6	138	US-08-484-397A-15	Sequence 15, Appli
25	334	18.2	60	US-08-484-397A-28	Sequence 28, Appli
26	320	17.4	60	US-08-484-397A-34	Sequence 34, Appli
27	316	17.2	60	US-08-484-397A-37	Sequence 37, Appli

28	311	16.9	60	2	US-08-484-397A-33	Sequence 33, Appli
29	310	16.8	60	2	US-08-484-397A-35	Sequence 35, Appli
30	309	16.8	60	2	US-08-484-397A-31	Sequence 31, Appli
31	307	16.7	55	1	US-08-366-953A-36	Sequence 36, Appli
32	307	16.7	60	2	US-08-484-397A-29	Sequence 29, Appli
33	307	16.7	60	2	US-08-484-397A-36	Sequence 36, Appli
34	306	16.6	60	2	US-08-484-397A-30	Sequence 30, Appli
35	304	16.5	60	2	US-08-484-397A-32	Sequence 32, Appli
36	284	15.4	55	1	US-08-366-953A-41	Sequence 41, Appli
37	283	15.4	55	1	US-08-366-953A-42	Sequence 42, Appli
38	283	15.4	55	1	US-08-366-953A-43	Sequence 43, Appli
39	282	15.3	55	1	US-08-366-953A-39	Sequence 39, Appli
40	280	15.2	55	1	US-08-366-953A-37	Sequence 37, Appli
41	280	15.2	55	1	US-08-366-953A-44	Sequence 44, Appli
42	279	15.2	55	1	US-08-366-953A-38	Sequence 38, Appli
43	277	15.1	55	1	US-08-366-953A-40	Sequence 40, Appli
44	147.5	8.0	784	4	US-09-982-308B-23	Sequence 23, Appli
45	128	7.0	1196	3	US-08-881-706-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-746-883-5
; Sequence 5, Application US/08746883
; Patent No. 6093693
; GENERAL INFORMATION:
; APPLICANT: Julius, Michael H., Philipp, Dominic,
; APPLICANT: Alizadeh-Khiavi, Kamel
; TITLE OF INVENTION: B Cell Activation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,883
; FILING DATE: No. 6093693ember 18, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 47841/00008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-746-883-5

Query Match	100.0%	Score 1840;	DB 3;	Length 375;
Best Local Similarity	100.0%	Pred. No. 4.6e-184;		
Matches 356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	61	QYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRLEKLTLEDLKITGTMPPLPLEA	120	
Db	80	QYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSRLEKLTLEDLKITGTMPPLPLEA	139	

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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-428-817A-68

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Query Match	61.8%	Score 1136.5	DB 6	Length 366
Best Local Similarity	65.7%	Pred. No. 4.1e-88		
Matches 232	Conservative 40	Mismatches 74	Indels 7	Gaps 3
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Qy	63	YADTVKALRVRRLLTVGAAQVPAQLLVGALRVLAYSRLLKELTLEDLIKITGTWPPPLEATG	122	
Dd	78	FTDIKSLSLKELTVRAARIDSRILFGALRVLGISGLQELTLENLEVTGTATPPPLEATG	137	
Qy	123	LALSRLNRNVSWATGRSWLAELQWLKPGIKVLISIAQAHSPAFSEYQVRAPPALTSLDL	182	
Dd	138	PDNLILNRNVSWATRDADWLAEQLQWLKPGIKVLISIAQAHSLNFSCEQVRVPFALSTL	197	
Qy	183	SDNPGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHNSL	242	
Dd	198	SDNPGLGERGLHISALCPKFFTLQVLALRNAGMETPSPGVCSALAAARVOLQGLDLHNSL	257	
Qy	243	RATVNPAPRCWMSGALSNSLNSPAGLEQVPKGLPAKLRVLDLSCNRLNRAPQPPDELPEV	302	
Dd	258	RDAA--CAPSCDFWSQLNSLNSLTGLKQVPKGLPAKLSVLDDLNSNRLDRPSPDELPOV	315	
Qy	303	DNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLOQARGF	355	
Dd	316	GNLSLKGNPFL---DSSSHSKFNFSVVVTAGAPSSOAVSLSGTALLGLDGLF	365	

```

RESULT 13
US-10-891-105-6
; Sequence 6, Application US/10891105
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.
; APPLICANT: FILIPP, Dominik
; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
; TITLE OF INVENTION: LAIT/8CD14-PROTEIN
; FILE REFERENCE: 47841/00063
; CURRENT APPLICATION NUMBER: US/10/891,105
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US/09/721,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: PCT/CA99/00482
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: US 60/086,884
; PRIOR FILING DATE: 1998-05-27
; NUMBER OF SEQ ID NOS: 11

```

```

; SOFTWARE: wordperfect 9.0
; SEQ ID NO 6
; LENGTH: 366
; TYPE: prt
; ORGANISM: murine
US-10-891-105-6

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Query Match	61.8%;	Score 1136.5;	DB 6;	Length 366;
Best Local Similarity	65.7%;	Pred. No. 4.1e-88;		
Matches 232;	Conservative 40;	Mismatches 74;	Indels 7;	Gaps 3
Qy	3	PEPCELDDDFRCVCFNFSFEPQOWSEAPQCWSAVEVEETHAGGLNLEPPLKRVADADAPQ	62	
Db	20	PEPCELDEES--CSCNFSDPKPMSSAFNCUGAADVELYGGRSLEYLLKKRVDTTEADLGG	77	
Qy	63	YADTVKALRVRRLLTVGAAQVPAQLLVGALRVILVYSRLKELTLEDLKIITGTMPPPLEATG	122	
Db	78	FTDIINKSLSKRLTVRAARIPSRILFCALRVILGIGSQELTLENLEVTGTAPPPLEATG	137	
Qy	123	LALLSSLRNVSWATGRSWEIAEQQWLKPGLVKVLUSIAQAHSFAPSYEYOVRAFPALTSIDL	182	
Db	138	PDNLNLMNVSWATRDWIAELQQWLKPGLVKVLUSIAQAHSNFSCEQVRYFPALSTIDL	197	
Qy	183	SDNPGIGERGLMAALCPHKFPALQNLALRNTGMTPTGVCALAAAGVQPHSLDLSHNSL	242	
Db	198	SDNPEIGERGLISALCPKPTPTQVLNLRNAGMETTPGVCALAAARVOLQGLDLSHNSL	257	
Qy	243	RATVNFSAPRCMSSALNSLNFSPAGLEQVPGKGLPAKLRVLDDLSCNRLNRAFPQDELPEV	302	
Db	258	RDAA--GAPSCDWFSQLNSLNSFTGLKQVPGKGLPAKLSVLDDLNVNLRDNPSPDELQV	315	
Qy	303	DNITLDGNPFLVPGTALPHFGSMNSGVVPACARSTLSVGVSGLTILVLLQARGF	355	
Db	316	GNLSLKGNNPFL---DSFSHSEKFNSSVYVTAGAPSSOAVLSGTLIALLLGDRLF	365	

RESULT 14

```

US-10-281-478A-10
; Sequence 10, Application US/10281478A
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Johnson, Richard S.
; APPLICANT: Guo, Lin
; APPLICANT: Mahimkar, Rajeev M.
; APPLICANT: Peschon, Jacques J.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: TREATING DISEASES MEDIATED BY METALLOPROTEASE-SHED PROTEINS
; FILE REFERENCE: 3327-A
; CURRENT APPLICATION NUMBER: US/10/281,478A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-281-478A-10

```

	Query Match	61.8%	Score 1136.5	DB 6	Length 366
	Best Local Similarity	65.7%	Pred. No. 4.1e-88		
	Matches 232	Conservative 40	Mismatches 74	Indels 7	Gaps 3
QY	3	PEPCELDDDFRCVCFNFSEFPQDPSWSEAFQCVS	AVEVEIHAGGLNLEPFLKRVDAADAPRQ	62	
DB	20	PEPCELDEES--CSCNFSDPKPKWSSAFNC	LGAADEVLYGGRSLEVLLKRVDEADLQ	77	
QY	63	YADTVKALRVRRLTVGAAQVPAOLLGALRV	LAYSRLKELTLEOLKITGTMPPLLEATG	122	
DB	78	FTDIIKSLSKRLTVRAARIPSRILFGALRV	LGISGLQELTLENLVGTGAPPPLEATG	137	
QY	123	LALSSLRLRNVSWATGRSWIAELQOMLKPG	LKVLSIAQAHSPAFSEYQVRAFPALTS	182	
DB	138	PDNIINLRNVSWATRADWIAELQOMLKPG	LKVLSIAQAHSLNFSGROVRVFPALST	197	

GENERAL INFORMATION:
APPLICANT: JULIUS, Michael H.; FILIPP, Dominik;
ALIZADEH-KHIAVI, Kamei
TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
PROTEIN (CD14), ENCODING GENE AND APPLICATION
IN B CELL ACTIVATION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/734,149
FILING DATE: 15-Dec-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/313,177
FILING DATE: 18-May-1999
APPLICATION NUMBER: 08/746,883
FILING DATE: November 18, 1996
APPLICATION NUMBER: PCT/CA 97/00880
FILING DATE: November 18, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 47841/00047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-734-149-4

Query Match 72.2%; Score 1328.5; DB 6; Length 373;
Best Local Similarity 74.2%; Pred. No. 2.1e-104;
Matches 264; Conservative 32; Mismatches 55; Indels 5; Gaps 4;
QY 2 TPECELDDEDFRCVCFNFBPQDSEAFQVSAVEVEIHAGGLNLPFLKRVDDADPR 61
DB 22 TPECELDDEDFRCVCFNFBPQDSEAFQVSAVEVEIHAGGLNLPFLKRVDDADPR 79
QY 62 QYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEAT 121
DB 80 QYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 139
QY 122 GLALSSRLRLNVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTS 181
DB 140 GPALTTLTSLRLNVSWTPGKGLVLAISRLKELTLEDLKITGTMPPLPLEA 199
QY 182 LSNPGLGRLGMAALCPHKFPAIONALRLNTGMEPTGVCAALAAAGVPHSLDLSHNS 241
DB 200 LSNPGLGRLGMAALCPHKFPAIONALRLNTGMEPTGVCAALAAAGVPHSLDLSHNS 259
QY 242 LRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPALRVLDLSCNLRNAPQDPDELPE 301
DB 260 LRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPALRVLDLSCNLRNAPQDPDELPE 318
QY 302 VDNLTLDGNPFLVPGTALPHEGS-MNSGVVPACARSTLSVGVSTVLVLLQARGFA 356
DB 319 VDNLTLDGNPFLVPGTALPHEGS-MNSGVVPACARSTLSVGVSTVLVLLQARGFA 373

RESULT 11
US-10-891-105-7
Sequence 7, Application US/10891105
GENERAL INFORMATION:
APPLICANT: JULIUS, Michael H.
APPLICANT: FILIPP, Dominik
TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
TITLE OF INVENTION: LAIT/SCD14-PROTEIN
FILE REFERENCE: 47841/00063
CURRENT APPLICATION NUMBER: US/10/891,105
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US/09/721,904
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: PCT/CA99/00482
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: US 60/086,884
PRIOR FILING DATE: 1998-05-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Wordperfect 9.0
SEQ ID NO 7
LENGTH: 377
TYPE: PRT
ORGANISM: rabbit
FEATURE:
NAME/KEY: unsure
LOCATION: (14)
OTHER INFORMATION: Xaa = unknown
FEATURE:
NAME/KEY: unsure
LOCATION: (265)---(267)
OTHER INFORMATION: Xaa = unknown
FEATURE:
NAME/KEY: unsure
LOCATION: (269)
OTHER INFORMATION: Xaa = unknown
US-10-891-105-7

Query Match 72.1%; Score 1326.5; DB 6; Length 377;
Best Local Similarity 72.7%; Pred. No. 3.2e-104;
Matches 258; Conservative 34; Mismatches 62; Indels 1; Gaps 1;
QY 2 TPECELDDEDFRCVCFNFBPQDSEAFQVSAVEVEIHAGGLNLPFLKRVDDADPR 61
DB 22 TPECELDDEDFRCVCFNFBPQDSEAFQVSAVEVEIHAGGLNLPFLKRVDDADPR 81
QY 62 QYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 120
DB 82 QYADTVKALRVRLTVGAQVPAQLLVGALRVLAISRLKELTLEDLKITGTMPPLPLEA 141
QY 121 TGLALSSRLRLNVSWATGRSWLAELQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTS 180
DB 142 TGPALSTLSRLNVSWPKGAWLSELOQWLKPGKLVLSIAQAHSPAFSYEQVRAFPALTS 201
QY 181 LSNPGLGRLGMAALCPHKFPAIONALRLNTGMEPTGVCAALAAAGVPHSLDLSHN 240
DB 202 LSNPGLGRLGMAALCPHKFPAIONALRLNTGMEPTGVCAALAAAGVPHSLDLSHN 261
QY 241 LRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPALRVLDLSCNLRNAPQDPDELPE 300
DB 262 LRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPALRVLDLSCNLRNAPQDPDELPE 321
QY 301 EVDNLTLDGNPFLVPGTALPHEGS-MNSGVVPACARSTLSVGVSTVLVLLQARGF 355
DB 322 KVNLSLDGNPFLVPGTALPHEGS-MNSGVVPACARSTLSVGVSTVLVLLQARGF 376

RESULT 12
US-10-428-817A-68
Sequence 68, Application US/10428817A
GENERAL INFORMATION:
APPLICANT: TERMAN, David S

; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/582,609
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2787
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-582-609-2787

Query Match 99.5%; Score 1831; DB 7; Length 375;
Best Local Similarity 99.7%; Pred. No. 5e-147;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEPECELDDEDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 20 TTEPECELDDEDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79

QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 120
DB 80 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 139

QY 121 TGLALSSLRNRVSWATGRSWLAELQWLKPGKLVLSIAQAHSFASVEQVRAFPALTSL 180
DB 140 TGLALSSLRNRVSWATGRSWLAELQWLKPGKLVLSIAQAHSFASVEQVRAFPALTSL 199

QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 259

QY 241 SLRATVNSAPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 300
DB 260 SLRATVNSAPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 319

QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOGARGFA 375

RESULT 8
US-10-432-236A-1
; Sequence 1, Application US/10432236A
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji
; APPLICANT: SHIRAKAWA, Kamon
; APPLICANT: MORI, Sadao
; TITLE OF INVENTION: ANTI CD14 MONOCLONAL ANTIBODY HAVING AN EFFECT OF INHIBITING CD14
; TITLE OF INVENTION: BINDING
; FILE REFERENCE: 1110-0315P
; CURRENT APPLICATION NUMBER: US/10/432,236A
; CURRENT FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-432-236A-1

Query Match 99.3%; Score 1827; DB 6; Length 356;
Best Local Similarity 99.4%; Pred. No. 1e-146;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEPECELDDEDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 1 TTEPECELDDEDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60

QY 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 120
DB 61 ROYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 120

QY 121 TGLALSSLRNRVSWATGRSWLAELQWLKPGKLVLSIAQAHSFASVEQVRAFPALTSL 180

DB 121 TGLALSSLRNRVSWATGRSWLAELQWLKPGKLVLSIAQAHSFASVEQVRAFPALTSL 180
QY 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
DB 181 DLSNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 240
QY 241 SLRATVNSAPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 300
DB 241 SLRATVNSAPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 300
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOGARGFA 356
DB 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOGARGFA 356

RESULT 9
US-10-891-105-4
; Sequence 4, Application US/10891105
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.
; APPLICANT: FILIPP, Dominik
; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
; TITLE OF INVENTION: LAIT/SCD14-PROTEIN
; FILE REFERENCE: 47841/00063
; CURRENT APPLICATION NUMBER: US/10/891,105
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US/09/721,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: PCT/CA99/00482
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: US 60/086,884
; PRIOR FILING DATE: 1998-05-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Wordperfect 9.0
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: bovine
US-10-891-105-4

Query Match 72.2%; Score 1328.5; DB 6; Length 373;
Best Local Similarity 74.2%; Pred. No. 2.1e-104;
Matches 264; Conservative 32; Mismatches 55; Indels 5; Gaps 4;

QY 2 TTEPECELDDEDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 61
DB 22 TTEPECELDDEDFRCVNFSEPPQDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79

QY 62 QYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 121
DB 80 QYADTVKALRVRLTVGAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLEA 139

QY 122 GLALSSLRNRVSWATGRSWLAELQWLKPGKLVLSIAQAHSFASVEQVRAFPALTSL 181
DB 140 GPALTTLNLRVSWATGRSWLAELQWLKPGKLVLSIAQAHSFASVEQVRAFPALTSL 199

QY 182 LSDNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 241
DB 200 LSDNPGGLGERGLMAALCPHKFPAIQNALRNTGMTPTGVCALAAAGVQPHSLDLSHN 259

QY 242 LRATVNSAPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 301
DB 260 LRATVNSAPRCMWSALNSLSFAGLEQVPGKLPKLRVLDLSCNRLNRAPOPDEL 318

QY 302 VDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOGARGFA 356
DB 319 VDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGSVGTLLVLOGARGFA 373

RESULT 10
US-10-734-149-4
; Sequence 4, Application US/10734149

; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-734-149-5

Query Match 100.0%; Score 1840; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TTPEPCELDDEDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 20 TTPEPCELDDEDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 120
DB 80 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 139
QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAFPALTSL 180
DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQAHSPAFSVEQVRAFPALTSL 300
DB 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQAHSPAFSVEQVRAFPALTSL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLOGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLOGARGFA 375
```

RESULT 5

PCT-US03-24918A-460

; Sequence 460, Application PC/TUS0324918A

; GENERAL INFORMATION:

; APPLICANT: GENECAST, INC.

; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS

; FILE REFERENCE: 49076.000004.PCT2

; CURRENT APPLICATION NUMBER: PCT/US03/24918A

; CURRENT FILING DATE: 2003-07-26

; PRIOR APPLICATION NUMBER: 10/207,655

; PRIOR FILING DATE: 2002-07-25

; PRIOR APPLICATION NUMBER: 10/053,530

; PRIOR FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: 60/367,358

; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/385,691

; PRIOR FILING DATE: 2002-06-03

; NUMBER OF SEQ ID NOS: 704

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 460

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-24918A-460

Query Match 99.5%; Score 1831; DB 1; Length 375;
Best Local Similarity 99.7%; Pred. No. 5e-147;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TTPEPCELDDEDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 20 TTPEPCELDDEDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 120
DB 80 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 139
```

```
QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAFPALTSL 180
DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQAHSPAFSVEQVRAFPALTSL 300
DB 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQAHSPAFSVEQVRAFPALTSL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLOGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLOGARGFA 375
```

RESULT 6

US-10-170-205E-22096

; Sequence 22096, Application US/10170205E

; GENERAL INFORMATION:

; APPLICANT: ADAMS, Mark

; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN

; FILE REFERENCE: CL001381

; CURRENT APPLICATION NUMBER: US/10/170,205E

; CURRENT FILING DATE: 2002-06-13

; NUMBER OF SEQ ID NOS: 40312

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 22096

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-170-205E-22096

Query Match

Best Local Similarity 99.5%; Score 1831; DB 6; Length 375;

Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TTPEPCELDDEDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
DB 20 TTPEPCELDDEDFRCVCFSEPDWSEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
QY 61 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 120
DB 80 ROYADTVKALVRRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDKLTGTMPPLPLEA 139
QY 121 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAFPALTSL 180
DB 140 TGLALSSRLRNVSATGRSWLAELQWLKPKLVLSIAQAHSPAFSVEQVRAFPALTSL 199
QY 181 DLSNPGGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
DB 200 DLSNPGGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 259
QY 241 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQAHSPAFSVEQVRAFPALTSL 300
DB 260 SLRATVNPSPRCMWSALNSLNSFAGLEQVPGKLPKLVLSIAQAHSPAFSVEQVRAFPALTSL 319
QY 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLOGARGFA 356
DB 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVSGTLLVLOGARGFA 375
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RESULT 7

US-60-582-609-2787

; Sequence 2787, Application US/60582609

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,


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RESULT 2
US-09-807-709D-1
; Sequence 1, Application US/09807709D
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; TITLE OF INVENTION: PROTEIN FOR TREATMENT OR PREVENTION OF G.I. TRACT DISORDER
; FILE REFERENCE: 113308-002
; CURRENT APPLICATION NUMBER: US/09/807,709D
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/EP99/07911
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: EP98203501.6
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-709D-1

Query Match      100.0%; Score 1840; DB 5; Length 356;
Best Local Similarity 100.0%; Pred. No. 8.1e-148;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPEPCELDDDEDFRCVNFSEPPQDMSAEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 1 TTPEPCELDDDEDFRCVNFSEPPQDMSAEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Qy 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
Dc 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
Qy 121 TGLALSRLRNVSWSATGRSWLAELQWLKPKGLKVLISIAQHSAPFSYEQVRAPFALTSL 180
Db 121 TGLALSRLRNVSWSATGRSWLAELQWLKPKGLKVLISIAQHSAPFSYEQVRAPFALTSL 180
Qy 181 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
Db 181 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
Qy 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
Db 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356

RESULT 3
US-10-891-105-5
; Sequence 5, Application US/108911105
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.
; APPLICANT: FILIPP, Dominik
; TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
; FILE REFERENCE: LAIT/SCD14-PROTEIN
; CURRENT APPLICATION NUMBER: US/10/891,105
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US/09/721,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: PCT/CA99/00482
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: US 60/086,884
; PRIOR FILING DATE: 1998-05-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Wordperfect 9.0
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
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; ORGANISM: human
US-10-891-105-5

Query Match      100.0%; Score 1840; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPEPCELDDDEDFRCVNFSEPPQDMSAEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 60
Db 20 TTPEPCELDDDEDFRCVNFSEPPQDMSAEAFQCVSAVEVEIHAGGLNLEPFLKRVDAADP 79
Qy 61 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 120
Db 80 RQYADTVKALRVRLTVGAAQVPAQLLVGALRVLAYSLKELTLEDLKITGTMPPLPLEA 139
Qy 121 TGLALSRLRNVSWSATGRSWLAELQWLKPKGLKVLISIAQHSAPFSYEQVRAPFALTSL 180
Db 140 TGLALSRLRNVSWSATGRSWLAELQWLKPKGLKVLISIAQHSAPFSYEQVRAPFALTSL 199
Qy 181 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 240
Db 200 DLSNPGLGERGLMAALCPHKFPAIONLALRNTGMETPTGVCALAAAGVQPHSLDLSHN 259
Qy 241 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 300
Db 260 SLRATVNPSPAPRCWSSALNSLNSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPOPDDEL 319
Qy 301 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 356
Db 320 EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA 375

RESULT 4
US-10-734-149-5
; Sequence 5, Application US/10734149
; GENERAL INFORMATION:
; APPLICANT: JULIUS, Michael H.; FILIPP, Dominik;
; APPLICANT: ALIZADEH-KHIAVI, Kamele
; TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
; PROTEIN (CD14), ENCODING GENE AND APPLICATION
; IN B CELL ACTIVATION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/734,149
; FILING DATE: 15-Dec-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/313,177
; FILING DATE: 18-May-1999
; APPLICATION NUMBER: 08/746,883
; FILING DATE: November 18, 1996
; APPLICATION NUMBER: PCT/CA 97/00880
; FILING DATE: November 18, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 47841/00047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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OM protein - protein search, using sw model

Run on: October 4, 2004, 16:53:41 ; Search time 74 Seconds
(without alignments)

759.304 Million cell updates/sec

Title: US-09-807-709D-1

Perfect score: 1840

Sequence: 1 TTPEPCLEDDDFRCVNF...TLVGSGTLLVQARGGPA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 838593 seqs, 157832909 residues

Total number of hits satisfying chosen parameters: 838593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pcp.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pcp.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pcp.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1840	100.0	356	US-09-807-709C-1	Sequence 1, Appli
2	1840	100.0	356	US-09-807-709D-1	Sequence 1, Appli
3	1840	100.0	375	US-10-891-105-5	Sequence 5, Appli
4	1840	100.0	375	US-10-734-149-5	Sequence 5, Appli
5	1831	99.5	375	PCT-US03-24918A-460	Sequence 460, App
6	1831	99.5	375	US-10-170-205E-22096	Sequence 22096, A
7	1831	99.5	375	US-60-582-609-2787	Sequence 2787, Ap
8	1827	99.3	356	US-10-432-236A-1	Sequence 1, Appli
9	1328.5	72.2	373	US-10-891-105-4	Sequence 4, Appli
10	1328.5	72.2	373	US-10-734-149-4	Sequence 4, Appli
11	1326.5	72.1	377	US-10-891-105-7	Sequence 7, Appli
12	1136.5	61.8	366	US-10-428-817A-68	Sequence 68, Appl
13	1136.5	61.8	366	US-10-891-105-6	Sequence 6, Appli
14	1136.5	61.8	366	US-10-281-478A-10	Sequence 10, Appl
15	1136.5	61.8	366	US-10-734-149-6	Sequence 6, Appli
16	297	16.1	72	US-10-793-479-4330	Sequence 4330, Ap
17	247	13.4	47	US-10-432-236A-2	Sequence 2, Appli
18	154	8.4	557	US-10-449-902-31160	Sequence 31160, A
19	152	8.3	613	US-10-425-115-277910	Sequence 277910, A
20	147.5	8.0	775	US-10-940-774-8799	Sequence 8799, Ap
21	147.5	8.0	784	US-10-732-796A-4	Sequence 4, Appli
22	147.5	8.0	784	US-10-170-205E-33662	Sequence 33662, A
23	147.5	8.0	784	US-10-760-620A-3558	Sequence 3558, Ap
24	147.5	8.0	784	US-10-760-320A-3558	Sequence 3558, Ap
25	147.5	8.0	784	US-60-582-609-2291	Sequence 2291, Ap
26	144.5	7.9	353	US-09-833-245A-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1

US-09-807-709C-1

; Sequence 1, Application US/09807709C

; GENERAL INFORMATION:

; APPLICANT: Nestec S.A.

; TITLE OF INVENTION: PROTEIN FOR TREATMENT OR PREVENTION OF G.I. TRACT DISORDER

; FILE REFERENCE: 113308-002

; CURRENT APPLICATION NUMBER: US/09/807,709C

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/EP99/07911

; PRIOR FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: EP98203501.6

; PRIOR FILING DATE: 1998-10-20

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 356

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-807-709C-1

Query Match	100.0%;	Score 1840;	DB 5;	Length 356;
Best Local Similarity	100.0%;	Pred. No. 8.1e-148;		
Matches	356;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	TTPEPCLEDDDFRCVNFSEPODMSAEFQCVSAVEVEIHAGGLNLEPFLKRVDAADP	60	
Db	1	TTPEPCLEDDDFRCVNFSEPODMSAEFQCVSAVEVEIHAGGLNLEPFLKRVDAADP	60	
QY	61	ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDIKITGTMPPLPLEA	120	
Db	61	ROYADTVKALRVRLTVGAAQVPAQLLVGALRVLAISRLKELTLEDIKITGTMPPLPLEA	120	
QY	121	TGLALSSLRNLNVSWATGSRWLAELOQWLKPGIKVLISIAQAHSFATSEYQVRAFPALTSL	180	
Db	121	TGLALSSLRNLNVSWATGSRWLAELOQWLKPGIKVLISIAQAHSFATSEYQVRAFPALTSL	180	
QY	181	DLSDNPLGELGRLMAALCPHKFPALQNLALRNTGMTPTGVCALAAAGVOPHSLDLSHN	240	
Db	181	DLSDNPLGELGRLMAALCPHKFPALQNLALRNTGMTPTGVCALAAAGVOPHSLDLSHN	240	
QY	241	SLRATVNSAPRCMWSALNSLNSFLAGLEQVFKGLPAKLRVLDSLNCNLRNAPQPDDEL	300	
Db	241	SLRATVNSAPRCMWSALNSLNSFLAGLEQVFKGLPAKLRVLDSLNCNLRNAPQPDDEL	300	
QY	301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPA CARSTLSVGVSGTLLVLOGARGFA	356	
Db	301	EVDNLTLDGNPFLVPGTALPHEGSMNSGVVPA CARSTLSVGVSGTLLVLOGARGFA	356	